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od List, per		SEQUENCE LISTING
2777		
(1)	GENERAL I	NFORMATION:
	(i)	APPLICANTS: BUKH, J., MILLER, R.H. AND PURCELL, R.H.
5	(ii)	TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
10	(iii)	NUMBER OF SEQUENCES: 263
15	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P. (B) STREET: 345 PARK AVENUE (C) CITY: NEW YORK (D) STATE: NEW YORK (E) COUNTRY: USA (F) ZIP: 10154
	(v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: FLOPPY DISK (B) COMPUTER: IBM PC COMPATIBLE (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: WORDPERFECT 5.1
20	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: TO BE ASSIGNED (B) FILING DATE: 26-MAY-1998
25	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 08/290,665 (B) FILING DATE: 15-AUG-1994
	(viii)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: 08/086,428 (B) FILING DATE 29-JUNE-1993
30	(ix)	ATTORNEY/AGENT INFORMATION: (A) NAME: RICHARD W. BORK (B) REGISTRATION NUMBER: 36,459 (C) REFERENCE/DOCKET NUMBER: 2026-4116US2
	(x)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (212) 758-4800 (B) TELEFAX: (212) 751-6849 (C) TELEX: 421792

0	(2) INFORMATION FOR (
5	(A) LI (B) TY (C) ST	CE CHARACTERISTICS: ENGTH: 576 base pairs YPE: nucleic acid FRANDEDNESS: single DPOLOGY: linear
3	(A) OF (C) II	AL SOURCE: RGANISM: homosapiens NDIVIDUAL ISOLATE: DK7
	(xi) SEQUENC	CE DESCRIPTION: SEQ ID NO:1:
10	AAT GAT TGC CCT AAC TGGAT GCC ATC CTG CAC ACC CCC ACG GTG GCC ACC ACC CAG CTT CGA CGT CAC ACC ACC CTC TGT TCG GCC CTC	CC ACG GGG CTT TAC CAT GTC ACC 39 CG AGT ATC GTG TAC GAG GCG GCC 78 CT CCG GGG TGT GTC CCT TGC GTT 117 CG AGG TGT TGG GTG GCG ATG ACC 156 CG GAT GGC AAA CTC CCC ACA GCG 195 CC GAT CTG CTC GTC GGG AGT GCC 234 CC TAC GTG GGG GAC CTG TGC GGG 273
15	AGG CGC CAC TGG ACG ACG TAT CCT GGC CAT ATA ACG ATG ATG AAC TGG TCGCT CAG ATC ATC GCT GGT GCT CAC TCG	GT CAA CTG TTT ACC TTC TCT CCC 312 CG CAA GGC TGC AAT TGT TCT ATC 351 CG GGT CAC CGC ATG GCG TGG GAT 390 CC CCT ACC ACG GCG TTG GTA GTA 429 CC CCG CAA GCC ATC TTG GAC ATG 468 CG GGA GTC CTG GCG GGC ATA GCG 507 CG AAC TGG GCG AAG GTC CTG GTA 546 CC GGC GTC GAC GCG 576
20	/2) INFORMATION FOR (TEO TE NO 2
	(2) INFORMATION FOR S	
25	(A) LE (B) TY (C) ST	CE CHARACTERISTICS: ENGTH: 576 base pairs YPE: nucleic acid FRANDEDNESS: single DPOLOGY: linear
	(A) OF	AL SOURCE: RGANISM: homosapiens NDIVIDUAL ISOLATE: DK9
	(xi) SEQUENC	CE DESCRIPTION: SEQ ID NO:2:
30	AAT GAT TGC CCT AAC TGGAT GCC ATC CTG CAT TGCCC ACG GTG GCC ACC ACC ACC ACC ACC ACC ACC ACC AC	CC TCG GGC CTC TAC CAT GTC ACC GG AGT ATT GTG TAC GAG GCG GCC TCCA GGG TGT GTC CCT TGC GTT CG AAA TGT TGG GTG GCG GCC GGC GAC GGC AAG CTC CCC GCA ACG GGAT CTG CTT GTC GGG AGC GCC TAT GTG GGG GAC TTG TGC GGG TAT GTG GGG GAC TTG TGC GGG
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5	AGA CGC CAC TGG ACA ATAC CCC GGC CAT ATT ATG ATG ATG AAC TGG CGC CAC CTC AGG ATC GCT GGT GCC CAC	GGC CAA CTG TTC ACC TTC TCC CCC 312 ACG CAA GAC TGC AAC TGT TCT ATC 351 ACG GGT CAT CGC ATG GCG TGG GAT 390 TCC CCT ACA GCA GCG CTG GTA ATG 429 ATC CCG CAG GCC ATC TTG GAC ATG 468 TGG GGA GTC CTA GCG GGC ATA GCG 507 GGG AAC TGG GCG AAG GTC GTG GTG ACC GGC GTC GAT GCG 576
	(2) INFORMATION FOR	SEQ ID NO:3:
10	(A) 1 (B) 5 (C) 8	NCE CHARACTERISTICS: LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
	(A) (NAL SOURCE: ORGANISM: homosapiens INDIVIDUAL ISOLATE: DR1
15	(xi) SEQUE	NCE DESCRIPTION: SEQ ID NO:3:
20	AAT GAT TGC CCT AAT TGAT GAT GCC ATC CTG CAC GCC ACG GTG GCC ACC ACC ACC ACC ACC ACC ACC ACC AC	CTC TAC GTG GGG GAC CTG TGC GGG 273 GGT CAA CTG TTC ACC TTT TCT CCC 312 ACG CAA GAC TGC AAT TGT TCT ATC 351 ACG GGA CAC CGT ATG GCA TGG GAT 390 FCC CCT ACG ACA GCG CTG GTA ATG 429 ATC CCA CAA GCC ATC TTG GAC ATG 468
25	ATC GCT GGA GCC CAC TAT TTC TCC ATG GTG CTG TTT C	GGG AAC TGG GCG AAG GTC GTG GTA 546
	(2) INFORMATION FOR	SEQ ID NO:4:
30	(A) I (B) 5 (C) 5	NCE CHARACTERISTICS: LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
35	(A) (NAL SOURCE: DRGANISM: homosapiens INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: CAC CAA GTG CGC AAC TCT ACA GGG CTT TAC CAT GTC ACC 39 AAT GAT TGC CCT AAT TCG AGT ATT GTG TAC GAG GCG GCC 78 GAT GCC ATC CTG CAC ACG CCG GGG TGT GTC CCT TGC GTT 117 CGC GAG GGT AAC ACC TCG AGG TGT TGG GTG GCG GTG ACC 156 5 CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG 195 CAG CTC CGA CGT CAC ATC GAC CTG CTT GTC GGG AGC GCC 234 ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG 273 TCT GTC TTC CTT GTC GGT CAA CTG TTC ACC TTC TCT CCC 312 AGG CAC CAC TGG ACA ACG CAA GAC TGC AAT TGT TCC ATC 351 TAT CCC GGC CAT ATA ACG GGC CAC CGC ATG GCG TGG GAT 390 ATG ATG AAC TGG TCC CCT ACG ACA GCG CTG GTA GTA GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG 468 10 ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG 507 TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA 546 GTG CTG TTG CTG TTT GCC GGC GTT GAT GCG 576 (2) INFORMATION FOR SEQ ID NO:5: 15 (i) SEQUENCE CHARACTERISTICS: LENGTH: 576 base pairs (A) (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: llinear (vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens 20 (C) INDIVIDUAL ISOLATE: SEQUENCE DESCRIPTION: SEQ ID NO:5: (xi) TAC CAA GTG CGC AAC TCC ACG GGG CTT TAC CAT GTT ACC 39 AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG ACA GCT 78 GAT GCT ATC CTA CAC GCT CCG GGA TGT GTC CCT TGC GTT 117 25 CGT GAG GGT AAC ACC TCG AGG TGT TGG GTG GCG ATG ACC 156 CCC ACG GTG GCC ACC AGG GAC GGG AAA CTC CCC GCA ACG 195 CAG CTT CGA CGT TAC ATC GAT CTG CTT GTC GGG AGC GCC 234 ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG TCT GTC TTT CTT GTC GGT CAG CT\$ TTT ACC TTC TCT CCC 312 AGG CGC CTC TGG ACG ACG CAA GAC TGC AAT TGT TCT ATC 351 TAT CCC GGC CAT ATA ACG GGT CAT CGC ATG GCA TGG GAT 390 ATG ATG AAC TGG TCC CCT ACG ACG GCA CTG GTA GTA 429 30 GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAT ATG 468 ATC GCT GGT GCT CAC TGG GGA GTC CTA GCG GGC ATA GCG 507 TAT TTC TCC ATG GTG GGA AAC TGG GCG AAG GTC CTA GTG 546 GTG CTG CTA TTC GCC GGC GTT GAC GCG 576 INFORMATION FOR SEQ ID NO:6:

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	(i) SEQU (A) (B) (C) (D)	STRANDEDNESS: single	
5	(vi) ORIG (A) (C)		
*	(xi) SEQU	JENCE DESCRIPTION: SEQ ID NO:6:	
10	AAT GAC TGC CCT AAC GAT ACC ATC CTA CAC CGC GAG GGT AAC GCC	TCG AGC ATT GTG TAC GAG ACG GCC TCT CCG GGG TGT GTC CCT TGC GTT TCG AGA TGT TGG GTG CCG GTG GCC TCG AGA TGT TGG GTG CCG GTG GCC	39 78 17 56
15	CAG CTT CGA CGT CAC ACC CTC TGC TCG GCC TCT GTC TTT CTT GTC AGG CGC CAC TGG ACA TAC CCC GGC CAT ATA ATG ATG ATG AAC TGG GCT CAG CTG CTC AGG ATC GCT GGT GCC CAC TAT TTC TCC ATG GCG	C ATC GAT CTG CTT GTT GGG AGC GCC C CTC TAT GTG GGG GAC CTG TGC GGG C AGC CAG CTG TTC ACT ATC TCC CCC A ACG CAA GAC TGC AAC TGT TCT ATC A ACG GGT CAC CGT ATG GCA TGG GAT C TCC CCT ACA ACG GCG TTG GTA ATA C GTC CCG CAA GCC GTC TTG GAC ATG C TGG GGA GTC CTA GCG GGC ATA GCG C GGG AAC TGG GCG AAG GTC CTG CTA	95 34 73 12 50 99 67 46
20	(2) INFORMATION FO	DR SEQ ID NO:7:	
25	(A) (B) (C) (D)	TYPE: nucleic acid STRANDEDNESS: single	
		JENCE DESCRIPTION: SEQ ID NO:7:	
30	TAC CAA GTA CGC AAC AAT GAT TGC CCT AAC GAT GCC ATT CTA CAC CGC GAG GAT GGC GCC CCC ACA GTC GCC ACT CAG CTT CGA CGT CAC	TCC TCG GGC CTT TAC CAT GTC ACC TCG AGT ATT GTG TAC GAG ACG GCC TCT CCA GGG TGT GTC CCT TGC GTT CCG AAG TGT TGG GTG GCC TAGG GAC GGC AAA CTC CCT GCA ACG TATC GAT CTG CTT GTC GGA AGC GCC	39 78 17 56 95 34
35	TCT GTC TTT CTC GTC		12

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5	TAT CCC GGC CAC ATA ACG GGATG ATG ATG ATG AAC TGG TCC CGGT CAC CAC TGG GGATC CAC TGGATC	AA GAC TGT AAC TGT TCT ATC GT CAC CGC ATG GCA TGG GAT CC ACA ACA GCG CTG GTA GTA CG CAA GCC GTC TTG GAC ATG GAC GTC CTA GCG GGC ATA GCG AC TGG GCG AAG GTC CTG ATA 546 GC GTC GAT GCG 576
	(2) INFORMATION FOR SEQ	ID, NO:8:
10		· ·
	(C) INDIV	ISM: homosapiens IDUAL ISOLATE: US11
15	(xi) SEQUENCE D	ESCRIPTION: SEQ ID NO:8:
20	AAT GAT TGC CCT AAC TCG AGGAT GCC ATC CTG CAC ACT CCGC GAG GGT AAC GCT TCG AGGCAA CTT CGA CCC ACG GTG GCC ACC AGG GACC ACC ATC GACC CTC TGT TCG GCC CTC TACT GTC GTC TCT GTC GCC CAC ACG CACA ACG ACG	GG TGT TGG GTG GCG ATG ACC AC GGC AAA CTC CCC ACA ACG AT CTG CTT GTC GGG AGC GCC AC GTG GGG GAC CTG TGC GGG AC CTG TTT ACC TTC TCT CCC AC GGC TGC AAT TGT TCT ATC AC GGC TGC ATG GCA TGG GAT AC CGC ATG GCA TGG GAT AC CAA GCC ATC TTG GTG GTA AC CTA GCG GGC ATA GCG AC TGG GCG AAG GTC CTG GTA AC TGG GCG AAG GTC CTG GTA AC TGG GCG AAG GTC CTG GTA 546
	(2) INFORMATION FOR SEQ	
30	(i) SEQUENCE CI (A) LENGTI (B) TYPE: (C) STRANI (D) TOPOLO	HARACTERISTICS: H: 576 base pairs nucleic acid DEDNESS: single DGY: linear
	(vi) ORIGINAL SO (A) ORGANI (C) INDIV	1
35	(xi) SEQUENCE DI	ESCRIPTION: SEQ ID NO:9:
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5	TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAT GTC ACG AAC GAC TGT TCC AAC TCG AGC ATT GTG TAT GAG ACA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG GAC AAC TCC TCT CGC TGC GTA GCG CTC ACC CCC ACG CTC GCG GAT CGC CTC ACC CCC ACG CTC GCG GAT CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TCC CAC GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TCC GCC ATG TAC GTG GGG GAT CTC TGC GGA TCT GTT TTC CTC ATC TCC CAG CTG TTC ACC CTC TCG CCT CGC CGG CAT GAG ACG GTA CAG GAG TGT AAT TGC TCA ATC TAT CCC GGC CAC GTG ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCA CCT ACA ACA GCC TTA GTG GTA TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC ATG GAC ATG GTG GCG GGC CTC GCC TAC TAT TCC ATG GGG GTC CTG GCC GGC CAC GTG ACA GCG GTC ATG GCT TTG GTA TTG GTG GCG GGC CTC GCC TAC TAT TCC ATG GGG GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GGG GAC TGG GCT AAG GTT TTG ATT GTG ATG CTC ATG GGG GTC CTG GCC GTG ATG CTC ATG GCC TAC TATG GTG GCG GGC CTC GCC TAC TAT TCC ATG GGG GTC CTG GCC GTG ATG GTG ATG GTG ATG GTG ATG GTG GTG	39 78 117 156 195 234 273 312 351 390 429 468 507 546 576
	(2) INFORMATION FOR SEQ ID NO:10:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
20	 (vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: D3 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: 	
25	TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAA GTC ACC AAT GAC TGT TCC AAC TCG AGC ATC GTG TAT GAG ACA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG GAC AAC TCC TCT CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCG GCT AGG AAT AGC AGC GTC CCC ACT ACG ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGC TCC GCC ATG TAC GTG GGG GAT CTT TGC GGA TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTC TCG CCT CGC CGG CAT GAG ACA GTA CAG GAA TGT AAC TGC TCA ATC TAT CCC GGC CAC GTG ACA GGT CAC CGC ATG GCT TGG GAT	39 78 117 156 195 234 273 312 351 390
30	ATG ATG AAC TGG TCG CCT ACA GCA GCC CTA GTG GTA TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAC TGG GGG GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT GGC GTC GAC GGC	429 468 507 546 576
	(2) INFORMATION FOR SEQ ID NO:11:	
35	(i) SEQUENCE CHARACTERISTICS:	
	372577_1	

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	(A) (B) (C) (D)	LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
5	(vi) ORIO (A) (C)		
	(xi) SEQ	UENCE DESCRIPTION: SEQ ID NO:11:	
10	AAC GAC TGC TCC AAC GAC GTG ATC ATG CAC CGG GAG AAC AAC CAC CCC ACG CTC GCG GCC ACA ATA CGA CGC CAC GCT TTC TGC TCC GCC	C TCA AGC ATC GTG TAT GAG GCA GTG 7 I ACC CCA GGG TGC GTG CCC TGC GTT 11 C TCC CGT TGC TGG GTA GCG CTC ACC 15 C AGG AAC GCC AGC ATC CCC ACT ACG 19 I GTC GAT TTG CTC GTT GGG GCG GCT 23 I ATG TAC GTG GGG GAC CTC TGC GGA 27	.7 .6 .5 .4 .73
15	CGC CGG CAT GAG ACT TAT CCC GGC CAC GTT ATG ATG ATG AAC TGC TCG CAG TTA CTC CGA GTG GCG GGG GCC CAC TAC TAC TCC ATG GCC	C TCT CAG CTG TTC ACC TTT TCA CCT A GCA CAG GAC TGC AAC TGC TCA ATC 35 F TCA GGT CAC CGC ATG GCT TGG GAT 39 G TCA CCT ACA ACA GCC CTA GTG CTA A ATC CCA CAA GCT GTC GTG GAC ATG C TGG GGA GTC CTG GCG GGC CTC GCC G GGG AAC TGG GCC AAG GTT TTA ATT 54 F GCC GGC GTT GAT GGG	51 90 29 58 97 6
20	(i) SEQU (A) (B)	STRANDEDNESS: single	
25	(vi) ORIC (A) (C)	GINAL SOURCE: ORGANISM: homosapiens INDIVIDUAL ISOLATE: HK3	
	(xi) SEQ	UENCE DESCRIPTION: SEQ ID NO:12:	
30	AAC GAC TGC TCC AAC GAC ATG ATC ATG CAT CGG GAG AAC AAC TCC CCC ACG CTC GCG GCC ACA ATA CGA CGT CAC GCC TTC TGC TCC GCT TCT GTT TTC CTT GTC CGC CGA CAC GAG ACA	C TCA AGC GTC GTG TAT GAG ACA GCA T ACC CCT GGA TGC GTG CCC TGC GTA 11 C TCC CGC TGT TGG GTA GCG CTC ACT C AGG AAC GTC AGC GTC CCC ACC ACG TGT GTC GAC TTG CTC GTT GGG GCG GCT ATG TAC GTG GGG GAT CTC TGC GGA A GTA CAG GAC TGC AAC TGC TCA CTC 35	7 6 5 4 3 2 1
35	TAT CCC GGC CAC GTZ	A TCA GGT CAC CGC ATG GCT TGG GAT 39	0
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	TCG CAA TTA CTC CGG AT GTG GCG GGG GCC CAC TG	C CCT ACA GCA GCC CTA G C CCG CAA GCT GTC GTG G G GGA GTC CTA GCG GGC C A AAC TGG GCT AAG GTT T C GGC GTT GAT GGG	AC ATG 468 TT GCC 507
5	(2) INFORMATION FOR S	EQ ID NO:13:	
10	(A) LE (B) TY (C) ST	E CHARACTERISTICS: NGTH: 576 base pairs PE: nucleic acid RANDEDNESS: single POLOGY: linear	
10	(A) OR	L SOURCE: GANISM: homosapiens DIVIDUAL ISOLATE: HK4	
	(xi) SEQUENC	E DESCRIPTION: SEQ ID N	0:13:
15	AAC GAC TGC TCC AAC TC. GAC ATG ATC ATG CAT AC CGG GAG AAC AAC TCC TC	A TCC GGG ATC TAC CAT G A AGT ATT GTG TAT GAG G C CCC GGG TGC GTG CCC T C CGT TGC TGG GTA GCG C	CA GCG 78 GC GTC 117 TC ACT 156
20	ACA ATA CGA CGC CAT GT GCT TTC TGC TCC GCC AT TCT GTC TTC CTC GTC TC CGC CGG CAT GAG ACG GT TAT CCC GGC CAC GTA TC ATG ATG ATG AAC TGG TC TCG CAG TTA CTC CGA CT GTG GCG GGA GCC CAC TG	G AAC GCC AGC ATC CCC A C GAC TTG CTC GTT GGG G G TAC GTG GGA GAT CTC T C CAG TTG TTC ACC TTC T A CAG GAC TGC AAT TGC T A GGT CAC CGC ATG GCT T A CCT ACA GCA GCC CTA G C CCA CAA GCT GTC ATG G G GGA GTC CTA GCG GGC C G AAC TGG GCC AAG GTT T C GGC GTT GAC GGG	CG GCT 234 GC GGA 273 CG CCT 312 CA ATC 351 GG GAT 390 TG GTA 429 AC ATG 468 TT GCT 507
25			
30	(A) LE: (B) TY: (C) ST: (D) TO: (vi) ORIGINA: (A) OR	EQ ID NO:14: E CHARACTERISTICS: NGTH: 576 base pairs PE: nucleic acid RANDEDNESS: single POLOGY: linear L SOURCE: GANISM: homosapiens DIVIDUAL ISOLATE: HK5	
	(xi) SEQUENC	E DESCRIPTION: SEQ ID N	O:14:
35	372577 1		

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5	AAC GAC TGC TCC AAC GAC ATG ATC ATG CAC CGG GAA AAC AAC TCC CCC ACG CTC GCG GCC GCA ATA CGA CGC CAC GCT TTC TGC TCC GCT TCT GTT TTC CTC GTC CGC CGA CAC GAG ACG TAT CCC GGC CAC GTA ATG ATG ATG AAC TGG GTA GCG GGG GCC CAC TAC TAT TCC ATG GTG	GTG TCC GGG GTA TAC CAT GTC ACG TTA AGC ATC GTG TAC GAG ACA ACG ACC CCT GGG TGC GTG CCC TGC GTT TCC CGT TGT TGG GTA GCG CTC GCC AGG AAC GCC AGC GTC CCC ACC ACG GTC GAC TTG CTC GTT GGG GCG GCT ATG TAC GTG GGG GAT CTT TGC GGA TCC CAG CTG TTC ACC TTC TCG CCT GTA CAG GAC TGC AAC TGC TCA ATC ACA GGT CAC CGC ATG GCT TGG GAT TCA CCT ACA ACA GCC CTA GTG GTG ATC CCG CAA GCT GTC GTG GAC ATG TGG GGG GTC CTG GCG GGC CTT GCC GGA AAC TGG GCT GAG GTT TTG ATT GCC GGC GTT GAT GGG	39 78 117 156 195 234 273 312 351 390 429 468 507 546 576
	(2) INFORMATION FO	R SEQ ID NO:15:	
15		ENCE CHARACTERISTICS: LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
	(vi) ORIG (A) (C)	INAL SOURCE: ORGANISM: homosapiens INDIVIDUAL ISOLATE: HK8	
20	(xi) SEQU	ENCE DESCRIPTION: SEQ ID NO:15:	
25	AAC GAC TGC TCC AAC GAC ATG ATT ATG CAT CGG GAG AAC AAC TCC CCC ACG CTC GCG GCT ACA ATA CGA CGC CAC	GTG TCC GGG ATA TAC CAT GTC ACG TCA AGC ATC GTG TAT GAA ACA GCG ACC CCT GGA TGC ATG CCC TGC GTT TCC CGT TGC TGG GTG GCG CTC ACT AGG AAT GTC AGC GTC CCC ACT ACG GTC GAC TTG CTC GTT GGG GCG GCT ATG TAC GTG GGG GAT CTC TGC GGA	39 78 117 156 195 234 273
	TCT GTT TTC CTC GTC CGC CGA CAC GAG ACG TAT CCC GGC CAC GTA ATG ATG AAC TGG TCG CAG TTA CTC CGG GTG GCC GAC	TCC CAG CTG TTC ACC TTT TCG CCT GTA CAG GAC TGC AAC TGC TCA ATC TCA GGT CAC CGC ATG GCT TGG GAT TCG CCC ACA ACA GCC CTA GTG GTG ATC CCG CAA GCT ATC GTG GAC ATG TGG GGA GTC CTA GCG GGC CTT GCC GGC AAC TGG GCT AAG GTT TTG ATT	312 351 390 429 468 507
30	GTG ATG CTA CTG TTT	CC GGC GTT GAT GGG	546 576
		R SEQ ID NO:16:	
	(i) SEQU (A)	ENCE CHARACTERISTICS: LENGTH: 576 base pairs	4
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	(B) (C) (D)	STRANDEDNESS: single
5	(vi) ORI (A) (C)	
	(xi) SEQ	UENCE DESCRIPTION: SEQ ID NO:16:
10	AAC GAC TGC TCC AA GAC ATG ATC ATG CA CGG GAG GGC AAC TC CCC ACT CTC GCG GC ACA ATA CGA CAC CA GCT TTC TGT TCC GC TCT GTT TTC CTC GT CGC CGG CAT GAG AC	C GTG TCC GGG GTG TAC CAT GTC ACG C TCA AGT ATT GTG TAT GAG GCA GCG C ACT CCC GGG TGC GTG CCC TGC GTT C TCT CGC TGC TGC GTA GCG CTC ACT C AGG AAC GCC AGC GTC TCC ACC ACG C GTC GAT TTG CTC GTT GGG GCG GCT C GTC GAT TTG CTC GTT GGG GCG GCT C TCC CAG CTG TTC ACC TTC TCA CCG C TCC CAG CTG TTC ACC TTC TCA CCG C TCC CAG CTG TTC ACC TTC TCA CCG C TCA GAC GAC TGC AAT TGC TCC ATC C TCA GGT CAC CGC ATG GCC TGG GAT C TCA GGT CAC CGC ATG GCC TGG GAT C TCA GGT CAC CGC ATG GCC TGG GAT C TCA GGT CAC CGC ATG GCC TGG GAT C TCA GGT CAC CGC ATG GCC TGG GAT C TCA GGT CAC CGC ATG GCC TGG GAT C TCA GGT CAC CGC ATG GCC TGG GAT C TCC TCC ATC C TCA GGT CAC CGC ATG GCC TGG GAT C TCC TCC ATC C TCC TCC ATC C TCC TCC ATC C TCC TCC ATC C TCC ATC
15	ATG ATG ATG AAC TG TCG CAG TTG CTC CG GTG GCG GGG GCC CA TAC TAT TCC ATG GT	G TCA CCT ACA GCA GCC CTA GTG GTA 429 G ATC CCA CAA GCT GTC GTG GAT ATG 468 C TGG GGA ATC CTG GCG GGC CTT GCC 507 A GGG AAC TGG GCT AAG GTT TTG ATT 546 T GCC GGC GTT GAC GGG 576
	(2) INFORMATION F	OR SEQ ID NO:17:
20	(i) SEQ (A) (B) (C) (D)	STRANDEDNESS: single
25	(vi) ORI (A) (C)	
	(xi) SEQ	UENCE DESCRIPTION: SEQ ID NO:17:
30	AAC GAC TGC TCC AA GAC ATG ATC ATG CA CGG GAG GGC AAC TT CCC ACT CTC GCG GC ACA ATA CGA CGC CA GCT TTC TGT TCC GC TCT GTT TTC CTT GT CGC CGG CAT GAG AC TAT CCC GGC CAC GT	C GTG TCC GGG GTG TAC CAT GTC ACG 39 C TCA AGT ATT GTG TAT GAG GCA GCG 78 C ACC CCC GGG TGC GTG CCC TGC GTT 117 C TCT AGT TGC TGG GTA GCG CTC ACT 156 T AGG AAC GCC AGC GTC CCC ACC ACG 195 C GTC GAT TTG CTC GTT GGG GCG GCT 234 T ATG TAC GTG GGG GAT CTC TGC GGA 273 C TCC CAG CTG TTC ACC TTC TCA CCG 312 A GTA CAG GAC TGC AAT TGC TCC ATC 351 A TCA GGT CAC CGC ATG GCT TGG GAT 390 G TCA CCT ACA GCG GCC CTA GTG GTA 429
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ŭ	TCG CAG TTG CTC CGG GTG GCG GGG GCC CAC TAC TAT TCC ATG GTA GTG ATG CTA CTC TTT	TGG GGA A	TC CTG GCG GG GG GCT AAG GT	C CTT GCC	468 507 546 576
5	(2) INFORMATION FO	R SEQ ID N	D:18:		
	(i) SEQUI (A) (B) (C) (D)	LENGTH: TYPE: nuc	CTERISTICS: 576 base pair cleic acid ESS: single linear	s	
10	(vi) ORIG (A) (C)	INAL SOURCI ORGANISM: INDIVIDUAI	homosapiens	10	
	(xi) SEQU	ENCE DESCR	PTION: SEQ I	D NO:18:	
15	TAT GAA GTG CGC AAC AAC GAC TGC TCC AAC GAC ATG ATA ATG CAC CGG GAG AAC AAC TCC	TCA AGT AT ACC CCC GC TCC CGC TC	TT GTG TAT GA GG TGC GTG CC GC TGG GTA GC	G GCA GCG C TGT GTT G CTC ACT	39 78 117 156
20	CCC ACA CTC GCG GCT GCA ATA CGA CGC CAT GCT TTC TGC TCC GCT TCT GTT CTC CTC GTC CGC CGG CAT TGG ACA TAT CCT GGC CAC GTA ATG ATG ATG AAC TGG TCG CAG CTA CTC CGG GTG GCG GGG GCC CAC TAC TAT TCC ATG GTG GTG ATG CTA CTC TTT	GTC GAT TO ATG TAC CAG CAG CAG CAG CAG CAG CAG CAG CAG C	AC TGC AAT TG AC CGC ATG GC CA GCA GCC CT AA GCT ATC TT CC CTG GCG GG GG GCT AAG GT	G GCG GCT C TGC GGA C TCA CCT T TCA ATC T TGG GAT A GTG GTG G GAT GTG C CTT GCC	195 234 273 312 351 390 429 468 507 546 576
25	(2) INFORMATION FOR	R SEQ ID NO):19:		
	(i) SEQUI (A) (B) (C) (D)	LENGTH: 5		s	
30	(vi) ORIG (A) (C)	INAL SOURCE ORGANISM: INDIVIDUAI	homosapiens		
	(xi) SEQUI	ence pescri	PTION: SEQ I	D NO:19:	
35	TAT GAA GTG CGC AAC	GTA TCC GC	GG GCG TAC CA	T GTC ACG	39
	372577_1				

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5	AAC GAC TGC TCC AAC TCA AGT ACT GTG TAC GAG GCA GCG GAC GTG ATC ATG CAT ACC CCC GGG TGT GTA CCC TGC GTT CAG GAG GGT AAC TCC TCC CAA TGC TGG GTG GCG CTC ACC CCC ACG CTC GCG GCC AGG AAC ATA CGA CGT CAT GTC GAT TTG CTC GTT TTC TGC TCC GCT ATG TAC GTG GGG GAC CTG TGC GGA TCT GTT TTC CTC ATC TCC CAG CTG TCC ACC ACC ACG CGT CGG CAT GAG ACA GTA CAG AAC TGC ATC TCG CCC CGT CGG CAT GAG ACA GTA CAG AAC TGC AAT TGC TCA ATC TAT CCC GGA CAC GTG ACA GGT CAT CGC ATG GCC TGG GAT ATG ATG ATG ATC CCA GAG GCC CTA GTG GCC TGG GAT ACA ACA GCC CTA GTG GTA CAG ACC TGT GCC GCC TAC TAT TCC ATG GGG ACC CTG GCC GCC TAC TAT TCC ATG GGG AAC TGG GCT AAG GTT TTG ATT GCT ATG CTA CTT TTT GCT GGT GTT GAC GGG	78 117 156 195 234 273 312 351 390 429 468 507 546 576
	(2) INFORMATION FOR SEQ ID NO:20:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (vi) ORIGINAL SOURCE:	
	(A) ORGANI\$M: homosapiens (C) INDIVIPUAL ISOLATE: S45	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
	TAT GAA GTG CGC AAC GTG TCC GGG GCG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA GTG GAC GTG ATC CTG CAC ACC CCT GGG TGC GTG CCC TGC GTT CGG GAG AAC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC AGG AAC TCC AGC GTC CCC ACT ACG ACA ATA CGA CGT CAC GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA	39 78 117 156 195 234 273
25	TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCG CCT CGT CGG CAT GAG ACA GTA CAG GAC TGC AAC TGT TCA ATC TAT CCC GGC CAC GTA ACA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA GCA GCC TTA GTG GTA TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT CTG ATT	312 351 390 429 468 507 546
30	GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG	576
	(2) INFORMATION FOR SEQ ID NO:21:	
	(i) SEQUENCE CHARACTERISTICS:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid	

		- 93 -	
0			
	(C) (D)		
	(vi) ORIO (A) (C)		
5	(xi) SEQ	UENCE DESCRIPTION: SEQ ID NO:21:	
10	AAC GAC TGC TCC AAC GAC ATG ATC ATG CAC CGG GAG AAC AAC TCC CCC ACG CTC GCG GCC ACA ATA CGA CGC CAC GCT TTC TGC TCC GCC TCT GTT TTC CTT GTC CGC CGG TAT GAG ACC TAT CCC GGC CGC GTC	C TCA AGC ATT GTG TAT GAG GCA GCG C ACC CCC GGG TGC GTG CCC TGC GTT C TCC CGC TGC TGG GTA GCG CTC ACT C AGG AAC TCC AGC GTC CCC ACT ACG C GTC GAT TTG CTC GTT GGG GCG GCT C ATG TAC GTG GGG GAC CTC TGC GGA C TCC CAG CTG TTC ACC TTC TCG CCT A GTA CAG GAC TGC AAT TGC TCA ATC A ACA GGT CAC CGC ATG GCT TGG GAT	39 78 17 56 95 34 73 12 59 29
15	GTG GCG GGG GCC CACTAC TAT TCC ATG GTC	G ATC CCA CAA GCT ATC GTG GAC ATG 46 C TGG GGA GTC CTA GCG GGC CTT GCC 50 G GGG AAQ TGG GCT AAG GTT TTG ATT 54	68 07 46 76
	(2) INFORMATION FO	OR SEQ ID NO:22:	
20	(i) SEQU (A) (B) (C) (D)	TYPE: nucleic acid	
25	(vi) ORIC (A) (C)	GINAL SOURCE: ORGANISM: homosapiens INDIVIDUAL ISOLATE: SW2	
25	(xi) SEQ	UENCE DESCRIPTION: SEQ ID NO:22:	
30	AAC GAC TGT TCC AAC GAC ATG ATC ATG CAC CGG GAG GCC AAC TCC CCC ACG CTA GCA GCC ACA ATA CGA CGC CAC GCT TTC TGC TCC GTC TCT GTT TTC CTC GTC CGC CGG CAC GAG ACC ATG ATG ATG AAC TGC	C TCA AGC ATT GTG TAT GAG ACA GCG T ACC CCC GGG TGC GTG CCC TGC GTT C TCC CGC TGC TGG GTA GCG CTC ACT C AGG AAC ACC AGC GTC CCC ACT ACG C GTC GAT TTG CTC GTT GGG GCG GCT T ATG TAC GTG GGG GAT CTC TGC GGA C TCC CAG CTG TTC ACT TTT TCA CCT A GTA CAG GAC TGC AAC TGT TCC ATC A TCA GGT CAC CGC ATG GCT TGG GAC G TCA CCT ACA GCA GCC CTG GTG GTA	39 78 17 56 93 12 50 92 8
35	372577_1		

0	GTA GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCA	507
	TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT GGC GTT GAC GGG	546 576
	(2) INFORMATION FOR SEQ ID NO:23:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: T3	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
15	TAC GAA GTG CGC AAC GTG TCC GGG GTG TAC TAT GTC ACG AAC GAC TGT TCC AAC TCA AGC ATT GTG TAT GAG ACA GCG GAC ATG ATC ATG CAC ACC CCT GGG TGC GTG CCC TGC GTT CGG GAG AGC AAT TCC TCC CGC TGC TGC GTA GCG CTT ACT CCC ACG CTC GCG GCC AGG AAC GCC AGC GTC CCC ACT AAG ACA ATA CGA CGT CAC GTC GAC TTG CTC GTG GGG GCG	39 78 117 156 195 234
20	GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA TCT GTT TTC CTC GTC TCC CAG CTG TTC ACT TTC TCG CCT CGC CGG CAT GAG ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAC GTA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCC ACA ACG GCA CTA GTG GTG TCG CAG TTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG CTG CTA CTC TTT GCC GGC GTT GAT GGG	273 312 351 390 429 468 507 546 576
25	(2) INFORMATION FOR SEQ ID NO:24:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: T10	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
35	TAT GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TTT GAG GCA GCG	39 78
	372577_1	

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5	CGG GAG GGC A CCC ACG CTC G ACG ATA CGA C GCT TTC TGC T TCT GTT TTC C CGC CGG CAT G TAT CCC GGC C ATG ATG ATG A TCG CAG TTA C GTG ACA GGG G TAC TAT TCC A	AAC TCC TCC CCC GCG GCC AGG AAC CGC CAT GTC GAT CCC GCT ATG TAT CTC GTC TCT CAG GAG ACT TTG CAG CAT CTG TCA GGT AAC TGG TCG CCT CTC CGG ATC CCA GCC CAC TGG GGA	GGG TGC GTG CCC TGC GTT TGC TGG GTA GCG CTC ACT ACC AGC GTC CCC ACT ACG TTG CTC GTT GGG GCG GCT GTG GGA GAC CTC TGC GGA CTG TTC ACC TTC TCG CCT GAC TGC AAC TGC TCA ATC GAC CGC ATG GCT TGG GAC ACA ACA GCT CTA GTG GTG CAA GCT GTC ATG GAC ATG CAA GCT GTC ATG GAC ATG GTC CTG GCG GGC CTT GCC TGG GCT AAG GTT TTA ATT S4 GTT GAT GGG 11 11 12 13 14 15 15 16 17 17 18 18 19 19 19 19 19 19 19 19
10	(2) INFORMAT	TION FOR SEQ ID	NO:25:
15	(i) (vi)	(C) STRANDEI (D) TOPOLOGY ORIGINAL SOUR (A) ORGANISM	576 base pairs ucleic acid NESS: single : linear CE:
	(xi)		RIPTION: SEQ ID NO:25:
	(XI)	DEGOENCE DESC	RIFITON. BEQ ID NO.25.
20	AAC GAC TGC TGAC ATG ATG	CC AAC TCA AGC ATG CAC ACT CCC	GGG ATG TAC CAT GTC ACG ATT GTG TAT GAG GCA GCG GGG TGC GTG CCC TGT GTT 11
20	AAC GAC TGC TGAC ATG ATG AAC AAC AAC AAC AAC AAC AAC AAC AAC AA	TCC AAC TCA AGC ATG CAC ACT CCC AAT TCC TCC CGC GCG GCC AGG AAC CCC CAC GTC GAT TCC GCT ATG TAC CTC ATC TCC CAG GAG ACA GTA CAG CAC GTA TCA GGT AAT TGG TCA CCT CTC CGG ATC CCA GCC CAC TGG GGA ATG GTG GGG AAC	ATT GTG TAT GAG GCA GCG GGG TGC GTG CCC TGT GTT TGC TGG GTA GCG CTC ACT GCT AGC GTC CCC ACT ACG 19 TTG CTC GTT GGG GCG GCT CTG GGG GAC CTC TGC GGG CTG TTC ACC TTC TCG CCT GAC TGC AAT TGT TCA ATC SAC CGC ATG GCT TGG GAT ACA GCA GCC CTA GTG GTA 42 CAA GCT GTC ATG GAC ATG 46 GTC CTG GCG GGC CTT GCC 50 TGG GCT AAG GTT CTG ATT 54
	AAC GAC TGC TGAC ATG ATG AAC AAC AAC AAC AAC AAC AAC AAC AAC AA	TCC AAC TCA AGC ATG CAC ACT CCC AAT TCC TCC CGC GCG GCC AGG AAC CCC CAC GTC GAT TCC GCT ATG TAC CTC ATC TCC CAG GAG ACA GTA CAG CAC GTA TCA GGT AAT TGG TCA CCT CTC CGG ATC CCA GCC CAC TGG GGA ATG GTG GGG AAC CTC TTT GCC GGC	ATT GTG TAT GAG GCA GCG GGG TGC GTG CCC TGT GTT TGC TGG GTA GCG CTC ACT GCT AGC GTC CCC ACT ACG TTG CTC GTT GGG GCG GCT GTG GGG GAC CTC TGC GGG CTG TTC ACC TTC TCG CCT GAC TGC AAT TGT TCA ATC GAC CGC ATG GCT TGG GAT ACA GCA GCC CTA GTG GTA ACA GCT GTC ATG GAC ATG GTC CTG GCG GGC TGG GCT AAG GTT CTG ATT S4 GTT GAC GGG 57
25	AAC GAC TGC TGAC ATG ATG AAC AAC AAC AAC AAC AAC AAC AAC AAC AA	TCC AAC TCA AGC ATG CAC ACT CCC AAT TCC TCC CGC GCG GCC AGG AAC CCC CAC GTC GAT TCC GCT ATG TAC CTC ATC TCC CAG GAG ACA GTA CAG CAC GTA TCA GGT AAT TGG TCA CCT CTC CGG ATC CCA GCC CAC TGG GGA ATG GTG GGG AAC	ATT GTG TAT GAG GCA GCG GGG TGC GTG CCC TGT GTT TGC TGG GTA GCG CTC ACT GCT AGC GTC CCC ACT ACG TTG CTC GTT GGG GCG GCT GTG GGG GAC CTC TGC GGG CTG TTC ACC TTC TCG CCT GAC TGC AAT TGT TCA ATC GAC CGC ATG GCT TGG GAT ACA GCA GCC CTA GTG GTA ACA GCT GTC ATG GAC ATG GTC CTG GCG GGC TGG GCT AAG GTT CTG ATT S4 GTT GAC GGG 57
25	AAC GAC TGC TGAC ATG ATG AAC AAC AAC AAC AAC AAC AAC AAC AAC AA	TCC AAC TCA AGC ATG CAC ACT CCC AAT TCC TCC CGC ECG GCC AGG AAC CGC CAC GTC GAT TCC GCT ATG TAC CTC ATC TCC CAG GAG ACA GTA CAG CAC GTA TCA GGT AAT TGG TCA CCT CTC CGG ATC CCA GCC CAC TGG GGA ATG GTG GGG AAC CTC TTT GCC GGC FION FOR SEQ ID SEQUENCE CHAP (A) LENGTH:	ATT GTG TAT GAG GCA GCG GGG TGC GTG CCC TGT GTT TGC TGG GTA GCG CTC ACT GCT AGC GTC CCC ACT ACG TTG CTC GTT GGG GCG GCT ACT GGG GCG GCT GTG GGG GAC CTC TGC GGG CTG TTC ACC TTC TCG CCT GAC TGC AAT TGT TCA ATC GAC TGC AAT TGT TCA ATC ACA GCA GCC CTA GTG GAT ACA GCA GCC CTA GTG GTA ACA GCT GTC ATG GAC ATG CTG GCG GGC CTT GCC TGG GCT AAG GTT CTG ATT S4 GTT GAC GGG NO:26: ACTERISTICS: 576 base pairs CCleic acid

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		(D) TOPOLOGY: linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: T2	
5	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:26:	
10	AAC GAC TGT TGC GCC GCG GTG GGA ACG CTC TGC TGC GGA ACG GTG ATG CGA CGC CAC TAC CCC GGT ACG ATG ATG ATG ATG ATG ATG GCG TAC GCG ACGC ACGC	AGG AAC ACC AGC CGC GGT TAC ATG GTG ACT CCC AAT GAG AGC A'TC ACC TGG CAG CTC CAA CTC CAC GTC CCC GGG TGT ATC CCG TGT GAG AAT ACA TCC CGA TGC TGG ATA CCG GTC ACA CCC GTG CGG CAG CCC GGC GCT CTT ACG CAG ACG CAC ATC GAC A'TG GTT GTG ATG TCC GCC CCT GCC CTC TAC GTG GGG GAC CTC TGC GGC CTC GCA GCC CAG A'TG TTC ATT GTC TCG CCG CTC GCA GCC CAG A'TG TTC ATT GTC TCC ATC ACC ATC ACT GGA CAC CGT ATG GCA TGG GAC ACC TGG TCG CCC A'CA GCC ACC ATG ATC CTG ATG CGC GTT CCC GAG GTC ATC ATA GAC ATC	39 78 117 156 195 234 273 312 351 390 429 468
15	TAC TTC TCT A	GCT CAC TGG GGC GTC ATG TTT GGC TTG GCC ATG CAG GGA GCG TGG GCG AAG GTC ATT GTC CTG GCT GCT GGG GTG GAC GCG	507 546 576
	(2) INFORMAT	CION FOR SEQ ID NO:27:	
20	(i) (vi)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear ORIGINAL SOURCE:	
20		(A) LENGTH: 576 base pairs (B) TYPE: pucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
20		(A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear ORIGINAL SOURCE: (A) ORGANISM: homosapiens	
	(vi) (xi) GCA CAA GTG A AAC GAC TGT T GCC GCG GTC C AAA ACG GGA A CCA AAC GTG G GGC TTG CGG A ACG CTC TGC T GGG GTG ATG C CAA CAT CAC T TAC CCT GGC A ATG ATG ATG A GCG TAC GCG A	(A) LENGTH: 576 base pairs (B) TYPE: pucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: T4	39 78 117 156 195 234 273 312 351 390 429 468 507

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o	TAC TTC TCT ATG CAG GGA GCG TGG GCG AAA GTC GTT GTC ATC CTT CTG GCC GCT GGG GTG GAC GCG	546 576
	(2) INFORMATION FOR SEQ ID NO:28:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: T9	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
15 20 25	GCC GAA GTG AAG AAC ACC AGT AGC AGC TAC ATG GTG ACA AAT GAC TGT TCC AAC GAC AGC ATC ACC TGG CAA CTC CAG GCC GCG GTC CTC CAC GTC CCC GGG TGC GTC CCG TGC GAG AGA GTT GGA AAC GCG TCG CGG TGC TGG ATA CCG GTC TCG CCA AAC GTA GCT GTG CAG CGG CCT GGC GCC CTC ACG CAG GGC TTG CGG ACG CAC ATC GAC ATG GTT GTG ATG TCC GCC ACG CTC TGC TCC GCT CTC TAC GTG GAG GAT CTC TGC GCC GGG GTA ATG CTC GCC GCT CAG ATG TTC ATT ATC TCG CCG CAG CAC CAC TGG TTT GTG CAG GAA TGC AAC TGC TCC ATT TAC CCT GGT ACC ATC ACT GGA CAC CGT ATG GAC ATG ATG ATG AAC TGG TCG CCC ACA ACC ACC ATG ATC TTC GCG GAG GCT CAC TGG GCC GTC ATC ATC AGC GGA GCT CAC TGG GCC GTC ATC ATC AGC GGA GCT CAC TGG GCC TAC TTC TCT ATG CAC GGA GCG GTC ATC ATA GAC ATC ATC CTG TTG CTC ACC GCT GGC GTG GCC (2) INFORMATION FOR SEQ ID NO:29: (i) SEQUENCE CHARACTERISTICS:	39 78 117 156 195 234 273 312 359 468 507 546 576
	(A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: US10	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
35	GTC CAA GTG AAA AAC ACC AGT ACC AGC TAT ATG GTG ACC AAT GAC TGC TCC AAC GAC ATC ACT TGG CAA CTT GAG GCT GCG GTC CTC CAC GTT CCC GGG TGT GTC CCG TGC GAG	39 78 117
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5	CCA AAT GTG GCC GTG GGC TTG CGG ACT CAC ACG CTC TGC TCC GCT GGG ATG ATG CTC GCA CGC CAC CAC TCG TTT TAC CCC GGT ACC ATC ATG ATG ATG AAC TGG GCG TAC GTG ATG CGC ATT AGC GGG GCG CAT TAC TTC TCT ATG CAG	G GTG CAG GAA TGC AAC TGC TCC ATC 351 C ACC GGG CAC CGT ATG GCA TGG GAC 390 G TCG CCC ACG GCC ACT TTG ATC CTG 429 C GTT CCC GAG GTC ATC ATA GAC ATC 468
10	(2) INFORMATION FO	OR SEQ ID NO:30:
	(i) SEQU (A) (B) (C) (D)	JENCE CHARACTERISTICS: LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
15	(vi) ORIG (A) (C)	GINAL SOURCE: ORGANISM: homosapiens INDIVIDUAL ISOLATE: DK8
	(xi) SEQU	JENCE DESCRIPTION: SEQ ID NO:30:
20	AAT GAT TGC TCA AAC GAC GCA GTT CTC CAC AAT GAC AAT GGC ACC CCT AAT GTG GCT GTG	C ATC AGT TCC AGC TAC TAC GCC ACC C AAC AGC ATC ACC TGG CAA CTC ACC C CTT CCC GGA TGC GTC CCA TGT GAG C CTG CGC TGC TGG ATA CAA GTG ACA C AAA CAC CGC GGC GCA CTT ACT CAT 195
25	ACG GTC TGC TCG GCC GCC GTG ATG ATC GTG GAA CGC CAC AAC TTT TAC CAA GGT CAT ATC ATG ATG CTA AAC TGG GCC TAT GCC GCT CGT GTC TTC GGC GGC CAT TAT TTC TCC ATG CAG	C GTC GAC GTG ATC GTA ATG GCA GCT C TTG TAT GTG GGA GAC GTA TGC GGG C TCG CAG GCT CTC ATA ATA TCG CCT C ACC CAG GAG TGC AAC TGT TCC ATC C ACC GGC CAC CGC ATG GCA TGG GAC C TCA CCA ACT CTT ACC ATG ATC CTC C GTT CCT GAG CTA GCC CTC CAG GTT C TGG GGC GTG GTG TTT GGC TTG GCC C GGA GCG IGG GCC AAA GTC ATT GCC C GCA GGA GTG GAT GCA C GCA GGA GTG GAT GCA 576
30	(2) INFORMATION FO	OR SEQ ID NO:31:
	(i) SEQU (A) (B) (C) (D)	JENCE CHARACTERISTICS: LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear

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	(vi) ORIC (A) (C)	GINAL SOURCE: ORGANISM: homosapiens INDIVIDUAL ISOLATE: DK11	
	(xi) SEQU	JENCE DESCRIPTION: SEQ ID NO:31:	
5	AAT GAT TGC TCA AAC AAC GCA GTT CTC CAC AAT GAC AAT GGC ACC CCT AAT GTG GCT GTC	C ACC AGT TCT AGT TAC TAC GCC ACC C AAC AGC ATC ACC TGG CAA CTC ACC C CTT CCC GGA TGC GTC CCA TGT GAG C CTG CAC TGC TGG ATA CAA GTG ACA C AAA CAC CGC GGC GCA CTC ACT CAC	39 78 117 156 195
10	ACG GTC TGC TCG GCC GCC GTG ATG ATC GTC TAC CAA GGT CAC ATC ATG ATG ATG GCC TAT GCC GCC CGT GTC TTC GGT GGT CAC ATG TAT TTC TCC ATG CAC	ATA GAT ATG ATT GTA ATG GCA GCT TTG TAT GTG GGA GAC GTG TGC GGG TCG CAG GCT TTC ATA GTA TCG CCA ACC CAA GAG TGC AAC TGT TCC ATC ACC GGC CAC CGC ATG GCA TGG GAC TCA CCA ACT CTC ACC ATG ATC CTC GTT CCT GAG CTA GTC CTT GAA GTC TGG GGT GTG GCC AAG GTC ATT GCC GGA GCG TGG GCC AAG GTC ATT GCC GCA GGA GTG GAT GCA	234 273 312 351 390 429 468 507 546 576
15			
13	(2) INFORMATION FO	OR SEQ ID NO:32:	
20	(i) SEQU (A) (B) (C) (D)	JENCE CHARACTERISTICS: LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
	(vi) ORIC (A) (C)	GINAL SOURCE: ORGANISM: homosapiens INDIVIDUAL ISOLATE: SW3	
	(xi) SEQU	JENCE DESCRIPTION: SEQ ID NO:32:	
25	AAT GAT TGC TCA AAC AAC GCA GTC CTC CAC AAT GAT AAT GGC ACC CCT AAT GTG GCT GTC AAC CTG CGA GCA CAC	C ATC AGT TCT AGC TAC TAT GCC ACC C AGC AGC ATC ACC TGG CAA CTC ACC C CTT CCC GGA TGC GTC CCG TGT GAG C CTG CAC TGC TGG ATA CAA GTG ACA G AAA CAC CGC GGC GCG CTC ACT CAC C GTC GAT ATG ATC GTA ATG GCA GCT C TTG TAT GTG GGA GAC ATG TGC GGG	39 78 117 156 195 234 273
30	GCC GTG ATG ATC GTG GAA CGC CAC AAC TTT TAC CAA GGT CGT ATC ATG ATG CTA AAC TGG GCC TAT GCC GCT CGT GTC TTC GGC GGC CAT TAT TTC TCC ATG CAA	TCG CAG GCT TTC ATA ATA TCG CCA ACC CAA GAG TGC AAC TGT TCC ATC ACC GGC CAC CGC ATG GCG TGG GAC TCA CCA ACT CTT ACC ATG ATC CTT GTT CCT GAG CTA GTC CTT GAA GTT TGG GGC GTG GTG TTT GGC TTG GCC GGA GCG TGG GCC AAG GTC ATT GCC	312 351 390 429 468 507 546
35	372577_1	C GCA GGA GTG GAT GCA	576
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	(2) INFORMATION FO	OR SEQ ID NO:33:
5	(A) (B)	STRANDEDNESS: single
	(vi) ORIG (A) (C)	
10	(xi) SEQU	JENCE DESCRIPTION: SEQ ID NO:33:
15	AAT GAT TGC TCG AAC AAC GCA GTT CTC CAC AAT GAC AAT GGC ACC CCT AAT GTG GCT GTG AAC CTG CGA ACG CAT ACG GTC TGC TCG GCC GCC GTG ATG ATA GCG GAA CGC CAC AAC TTC TAC CAA GGT CAT ATC	ACC AGT TTT AGC TAC TAC GCC ACC ACC AGT TTT AGC TAC TAC GCC ACC ACC AGC ATC ACC TGG CAG CTC ACC ACC CTT CCC GGA TGC GTC CCA TGT GAG TTG CGC TGC TGG ATA CAA GTA ACA AAA CAC CGT GGC GCA CTC ACT CAC GTC GAC GTG ATC GTA ATG GCA GCT TTG TAT GTG GGG GAC GTG TGC GGG TCG CAG GCT TTC ATA ATA TCG CCA ACC CAG GAG TGC AAC TGT TCC ATC ACC GGC CAC CGC ATG GCA TGG GAC 39
20	GCC TAC GCT GCT CGT GTC TTC GGC GGC CAT TAT TTC TCC ATG CAA	G TCA CCA ACT CTC ACC ATG ATC CTC 429 G GTG CCT GAA CTA GTC CTT GAA GTT 468 T TGG GGC GTG GTG TTT GGC TTG GCC 507 G GGA GCG TGG GCC AAA GTC ATC GCC 546 G GCA GGA GTG GAC GCA 576
	(2) INFORMATION FO	R SEQ ID NO:34:
25	(A) (B)	
	(vi) ORIG (A) (C)	INAL SOURCE: ORGANISM: homosapiens INDIVIDUAL ISOLATE: S83
30	(xi) SEQU	ENCE DESCRIPTION: SEQ ID NO:34:
35	AAC GAT TGC TCC AAC GGA GCA GTG CTT CAT CGT ACC GCC AAC GTC	ACC GGC GAC TCC TAC ATG CCG ACC TCT AGT ATC GTT TGG CAG CTT GAA ACT CCT GGA TGC GTC CCT TGT GAG TCT CGA TGT TGG GTG CCG GTT GCC AGT CAA CCT GGC GCT CTC ACT AAG 195
	372577_1	

0			
·	ACG GTC TGT GCG CTG ATG CAA CAC CAT TAC CCG GGC	TCT GCC CTT TCTG GCC GCT CCC GCC ATT ACG GCC	ATC ATC GTG ATG TCT GCT 234 TAT GTG GGG GAC GTG TGT GGC 273 TAG GTC GTC GTC TCG CCA 312 TAG GAA TGC AAC TGT TCC ATA 351 TGA CAC CGC ATG GCT TGG GAT 390
5	GCG TAC TTG GTT ACA GGA TAC TTC TCC	GTG CGC ATC C GGT CAT TGG G ATG CAG GGA T	CC ACT ACC ACC ATG CTC CTG 429 CG GAA GTC ATC TTG GAT ATT 468 GT GTA ATG TTT GGC CTC GCT 507 CG TGG GCG AAG GTC ATC GTT 546 GGG GTG GAG GCG 576
	(2) INFORMA	ATION FOR SEQ	ID NO:35:
10	(i)	(A) LENGT (B) TYPE: (C) STRAN	
15	(vi)	(C) INDIV	ISM: homosapiens IDUAL ISOLATE: DK12
	(xi)	SEQUENCE D	ESCRIPTION: SEQ ID NO:35:
20	AAC GAC TGT GAC GTC ATT CAG GAC GGC CCT ACA GTG TCG ATA CGC ACG ATG TGC GCC GTC TTC CGT CGC CAT	TCC AAT AGC A CTG CAC ACA C AAT ACA TCT A GCA GTC AGG T AGT CAT GTG G TCT GCG CTC T CTT GTG GGA C CAA ACA GTC C	CC GGC CTC TAC GTC CTT ACC GT ATC GTG TAT GAG GCC GAT 78 CT GGC TGT GTA CCT TGT GTT 117 CG TGC TGG ACC TCA GTG ACG AC GTC GGA GCA ACC ACC GCT AC CTG CTA GTG GGC GCC AC GTG GGT GAT GTG TGT GGG AC GTG GGT GAT GTG TGT GGG AC GCC TTC ACG TTC AGA CCT 39 39 31 32 34 35 36 36 36 37 36 36 37 36 36 37 37
25	ATG ATG ATG GCG CAC GTC ATA GCT GGG TAT TAC TCC	AAT TGG TCC CCTG CGT CTG CAT TGG GATG CAG GGC A	GA CAT CGA ATG GCT TGG GAT 390 CC GCT GTG GGT ATG GTG GTA 429 CC CAG ACC TTG TTC GAC ATA 468 GC ATC ATG GCG GGC CTA GCC 507 AC TGG GCC AAG GTC GCT ATC 546 GA GTC GAT GCC 576
	(2) INFORMA	ATION FOR SEQ	ID NO:36:
30	(i)	(A) LENGT	
	(vi)	ORIGINAL S (A) ORGAN	OURCE: ISM: homosapiens
35			
	372577_1		

0			
		(C) INDIVIDUA	L ISOLATE: HK10
	(xi)	SEQUENCE DESCR	IPTION: SEQ ID NO:36:
5	AAC GAC TGT CCC GAC GTC ATT CTC CAG GAC GGC AAT CCT ACA GTG GCA TCG ATA CGC AGT ACG ATG TGC TCT GCC GTC TTC CTC CGT CGC CAT CAA TAC CCA GGC CAC ATG ATG ATG ATG GCG CAC GTC CTC ATA GCC GGG GCC	C AAT AGC AGT AGC AGC AGC ACA CCT GG AGG TAC GG CTC TAC GG GTG GGA CAA GG ACG GTC CAG AGC CTT TCA GGA CG CGG TTG CCC GG CGC CAT TGG GGC AGC CAC ACC CAT TGG GGC AGC CAT TGG GGC AGC CAC ACC CAC ACC CAC ACC CAC ACC CAC CA	GC CTC TAT GTC CTT ACC 39 TT GTG TAT GAG GCC GAT 78 GC TGT GTA CCT TGT GTT GC TGG ACC TCG GTG ACA 156 TC GGA GCA ACC ACC GCC 195 TG TTA GTG GGC GCG 78 GC TGT AAC TGT GTG CC TTC ACG TTC AGA CCG CC TTC ACG TTC AGA CCG CC TGT AAC TGC TCG CTG AT CGA ATG GCT TGG GAT AG ACC TTG TTC GAC ATA 468 TC TTG GCA GGC CTA GCC 507 GG GCC AAG GTC GCT ATC
15	ATC ATG GTT ATC	STTT TCA GGG GEON FOR SEQUENCE CHARACE (A) LENGTH: 10 (B) TYPE: nucleon (C) STRANDEDN	CTERISTICS: 576 base pairs cleic acid ESS: single
20	(vi)	(D) TOPOLOGY: ORIGINAL SOURC (A) ORGANISM: (C) INDIVIDUA	linear
25	AAC GAC TGT TCC GAC GTT ATT CTC CAG GAC GGT AAT CCT ACA GTG GCA TCG ATA CGC AGT	C AAT AGC AGT A' C CAC ACA CCT GC ACA TCC ACG TC AGTC AGG TAT GT C CAT GTG GAC CT	GC CTC TAT GTC CTC ACC 39 TT GTG TAT GAG GCC GAT 78 GC TGT GTA CCT TGT GTT 117 GC TGG ACC CCA GTG ACA 156 TC GGA GCA ACC ACC GCT 195 TA TTG GTG GGC GCC 234
30	GCC GTC TTT CTC CGT CGC CAT CAA TAC CCA GGC CAT ATG ATG ATG AAT GCG CAC GTT CTC ATA GCC GGG GCC	C GTG GGA CAA GGA ACG GTC CAG ACG CTT TCA GGA CAG GCC CCC GCC CAT TTG CCC CAT TGG GGC ACG CAAA GCC AAC TCG	TG GGT GAT ATG TGT GGG 273 CC TTC ACG TTC AGA CCT 312 CC TGT AAC TGC TCG CTG 351 AT CGC ATG GCT TGG GAT 390 CT GTG GGT ATG GTG GTG 429 AG ACC GTG TTC GAC ATA 468 TC TTG GCG GGC CTA GCC 507 GG GCC AAG GTC GCT ATC 546 TC GAC GCC 576

	- 103 -	
	(2) INFORMATION FOR SEQ ID NO:38:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: S52	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
10	CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC GTC ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGC AAT ACA TCC ATG TGC TGG ACC CCA GTG ACA CCT ACG GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG GGC GCG ACG CTG TGC TCT GCG CTC TAT GTG GGT GAT ATG TGT GGG	39 78 117 156 195 234 273
15	GCC GTC TTT CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT GTT TCA GGA CAT ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG GCG CAC ATC CTG CGA TTG CCC CAG ACC TTG TTT GAC ATA CTG GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC TAT TAT TCT ATG CAG GGC AAC TGG GCC AAG GTC GCT ATT GTC ATG ATT ATG TTT TCA GGG GTG GAT GCC	312 351 390 429 468 507 546 576
20		
	(2) INFORMATION FOR SEQ ID NO 39:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: S54	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
30	CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT ATC CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC GTC ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGC AAT ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACG GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG GGC GCG GCC ACC GTG TGC GTG GCC GTG TATT GTG GGC GCG GCC	39 78 117 156 195 234
35	ACG CTG TGC TCT GCG CTC TAT GTG GGT GAT ATG TGT GGG	273

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5	GCC GTC TTT CTC GTC CGT CGC CAT CAA ACC TAC CCA GGC CAT CTT ATG ATG ATG AAT TGC GCG CAC ATC CTG CGA CTG GCC GGG GCC CAT TAT TAT TCT ATG CAC ATC ATG ATT ATG TTT	G GTC CAG ACC T TCA GGA CAT G TCC CCC GCT A TTG CCC CAG T TGG GGC ATC G GGC AAC TGG	TGT AAC TGC TCC CGA ATG GCT TGC GTG GGT ATG GTC ACC TTG TTT GAC TTG GCG GGC CTC GCC AAG GTC GCC	G CTG 351 G GAT 390 G GTG 429 C ATA 468 A GCC 507
	(2) INFORMATION FO	OR SEQ ID NO	40:	
10	(A) (B)	TYPE: nuclest strandedness	6 base pairs eic acid S: single	
	(vi) ORIC (A) (C)		homosapiens ISOLATE: Z4	
15	(xi) SEQU	JENCE DESCRIP	TION: SEQ ID NO	:40:
20	GAG CAC TAC CGG AAT AAT GAT TGT CCG AAT CAT CAC ATC CTA CAC ATG ACT GGG AAC ACA CCT ACA GTG GCT GTC TCG TTC CGG CGA CAT ACT TTG TGT TCT GCC GGT GCC TTC CTG ATC CGT CGC CAC TGG ACC TAC ACT GGC CAT ATC ATG ATG ATG AAC TGC GCC CAG ATC ATG AGC GTT GCC GGA GGC CAC TAC TTC AGC ATG CAA GTC CTT TTC CTC TTT	TCC AGT ATA TTG CCG GGG TGC CGT TGC GCA CAC CCG GTG GAC TTA CCTC TAT GTT GGG CAG ATG ACG CAG GAG ACC GGC CAC ACC GGC CAC GTC CCC ACA TGG GGC GTC AGC AGC ATG	GTC TAT GAA GCTGGC GTA CCC TGGGG GAC CTC TGGGGG GAC CTC TGGAGG ATG GCG ATG ATG ATG ATG ATG ATG ATG ATG ATG AT	F GAC 78 F GTG 117 G ACG 156 F GAG 195 G GCC 234 C GGA 273 G CCG 312 C ATC 351 G GAC 390 C CTC 429 C ATG 468 G GCG 507
	(2) INFORMATION FO			3,0
30	(A) (B) (C) (D)	TYPE: nuclest strandedness TOPOLOGY:	6 base pairs eic acid	
	(vi) ORIC (A) (C)		homosapiens ISOLATE: Z1	
35				

	(xi) SEQU	ENCE DESCRIPTION: SEQ ID NO:41:	
5	AAT GAT TGC CCT AAC CAC CAC ATC ATG CAC CGG ACG GAG AAT ACT CCC ACT GTG GCC GCG TCC ATG CGC AGG CAT ACT ATG TGT TCC GCC GGC GTC TTC CTA GTG CGC CGG CAC TGG ACC TAT CCT GGT CAC GTC ATG ATG ATG AAC TGG GCT CAG ATC TTA CGG CTC ACC GGG GGT CAC TTC TTC AGC ATG CAG	GCT TCG GGC GTC TAT CAT GTC ACC ACC AGC ATA GTG TAC GAG ACG GAG TTG CCA GGG TGT GTC CCC TGT GTG TCT CGC TGC TGG GTG CCC TTG ACC CCC TAT CCC AAC GCA CCG TTA GAG GTA GAC CTG ATG GTG GGT GCG GCT TTC TAC ATT GGA GAT CTG TGT GGA GGC CAG CTG TTC GAC TTC CGA CCG ACC CAG GAT TGC AAC TGC TCC ATC TCG GGC CAC AGG ATG GCC TGG GAC AGC CCT ACC AGC GCG CTG ATT ATG ATC CCC TCT ATC CTA GGT GAC TTG TGG GGA GTT CTT GCT GGT CTA GCT AGT AAC TGG GCG AAG GTC ATC CTG GCC GGG GTC GAG GGA	39 78 117 156 195 234 273 312 351 390 468 507 546
	•	R SEQ ID NO:42:	
15	(A) (B)	STRANDEDNESS: single	
20	(vi) ORIG (A) (C)	INAL SOURCE: ORGANISM: homosapiens INDIVIDUAL ISOLATE: Z6	
	(xi) SEQU	ENCE DESCRIPTION: SEQ ID NO:42:	
25	AAC GAC TGC CCG AAC CAC CAG ATC TTA CAC AGG GTT GGG AAT CAG CCC ACC GTG GCG GTG TCC CTC CGG AGA CAT ACT GTA TGC TCT GCC GGT GCA TTC TTG GTT	GCC TCG GC GTC TAT CAC GTC ACC TCG AGC ATA GTG TAT GAG GCC GAA CTC CCA GGG TGC TTG CCC TGT GTG TCA CGC TGC TGG GTG GCC CTT ACT TCT TAT ATC GGT GCT CCG CTT GAC GTG GAC CTG ATG GTG GGC GCC GCT CTC TAC GTT GGA GAT CTG TGC GGT GGC CAG ATG TTC TCC TTC CAG CCG ACG CAG GAC TGC AAT TGT TCT ATC	39 78 117 156 195 234 273 312 351
30	TAC GCA GGG CAT ATC ATG ATG ATG ATG AAC TGG GCC CAG GTC ATG AGG CTC GCT GGA GGG CAC TAC TTC AGT ATG CAA	ACG GGC CAC AGG ATG GCA TGG GAC AGT CCC ACA ACC ACC CTG CTT CTC ATC CCT AGC ACT CTG GTA GAT CTA TGG GGC GTC CTT GTT GGG TTG GCG GCT AAT TGG GCC AAA GTC ATC CTG GCT GGA GTT GAT GCC	390 429 468 507 546 576
	(2) INFORMATION FO	R SEQ ID NO:43:	

0			
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: Z7	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:43:	
10	AAC GAC TGC CC CAC CAC ATC CT AGG GAG GGG AA CCC ACC GTG GC TCC ATC CGG AG	C CAG TCA CGC TGC TGG GTG GCC CTT ACT G GCG CCT TAT ATC GGT GCA CCG CTT GAA A CAT GTG GAC CTG ATG GTA GGC GCT GCT	39 78 117 156 195 234 273
15	GGC GTA TTT TT CGA CGC CAC TG TAT GCG GGG CA ATG ATG ATG AA GCC CAG GTT AT CTC ACT GGA GG TAC TTC TGC AT	G GTT GGT CAG ATG TTT TCT TTC CAG CCG G ACT ACG CAG GAC TGC AAT TGT TCC ATC C GTT ACA GGC CAC AGA ATG GCA TGG GAC C TGG AGT CCC ACA ACC ACC TTG GTC CTC G AGG ATC CCT AGC ACT CTG GTG GAC CTA G CAC TGG GGT ATC CTT ATC GGG GTG GCA G CAA GCT AAT TGG GCC AAG GTC ATT CTG	312 351 390 429 468 507 546
20	(2) INFORMATI	ON FOR SEQ ID NO:44:	
20	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: DK13	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:44:	
30	AAC GAT TGC CC TAC CAC ATC TT AGG GAA GGG AA CCC ACC GTG GC TCT TTG AGA CG ACT CTC TGC TC GGT GTG TTC TT	C AAG TCT ACA TGC TGG GTG TCT CTC ACC T GCG CAA CAT CTG AAT GCT CCG CTT GAG T CAC GTG GAT CTG ATG GTG GGC GCC C GCC CTC TAC ATC GGA GAC GTG TGT GGG G GTC GGT CAA CTG TTC ACC TTC CAA CCT	39 78 117 156 195 234 273 312
35	372577_1		-

GTC CTG TTT CTC TTT GCT GGA GTC GAC GCT

TAC ACA GGA CAT ATC ACA GGA CAC AGA ATG GCT TGG GAC ATG ATG AAT TGG AGC CCC ACT GCG ACG CTG GTC CTC

GCC CAA CTT ATG AGG ATC CCA GGC GCC ATG GTC GAC CTG

CTT GCA GGC GGC CAC TGG GGC ATT CTG GTT GGC ATA GCG

TAC TTC AGC ATG CAA GCT AAT TGG GCC AAG GTT ATC CTG

390 429

468

507

546

576

39

78

156

195

234

273

312

351

390

429

468

507

546

576

(D)

(A)

(C)

TOPOLOGY:

ORIGINAL SOURCE:

linear

ORGANISM: homosapiens

SEQUENCE DESCRIPTION: SEQ ID NO:46:

INDIVIDUAL ISOLATE:

372577_1

(vi)

(xi)

30

5	AAT GAAAC CTAC ACC CT CTAC ACC CAATT GCAATT GCAATT TTAT	CC TAC AT TGC IG ATC AA GAT CG TTG IT CGG IT CGC IG TTT AG CAC GT GGC IG ATG AG TTG AG TTG IG GGG IG TTG IG GCG IG TTT	CCA TTG AAT TCA AGG TCC TTG ACT CAT AAT CTA GGC TCA	AAC CAT GCC GCC GCA GTA ACG ATC TGG CGG CAC	TCT GCA AGT CCG GTT CTA GGC GTG ACC TCA ATT TGG GCT	TCC CCT AAG AAT GAC CAA CAA CCT CCC GGG AAC	ATA GGT TGC CTC TAC GTC ATG GAC CAC ACG CAG GTC TGG	GTT TGC TGG GGA TTA GGG TTC CGG ACG GTG TTG GCT	TAC GTG GCG GCG GAC ACC AAT ATG GCC GTC TTT AAG	GAG CCT CAA GTC GGA GCG TAT TGC GCA TTG ATC GCC	GCT TGT ATC ACG GGG TGC AGG TCT TGG CTG GAC GCC	GAT GCC GCT GCT GGG CCT ATT GAC ATG ATC GCA	39 78 117 156 195 234 273 312 351 390 429 468 507 546 576
	(2)	INFORM	OITA	N FOF	R SEÇ	Q ID	NO:4	7:					
15	,	(i)		SEQUE (A) (B) (C) (D)	LENC TYPE STRA	STH:	576 nucle ONES	bas	se pa acid singl	airs			
		(vi)		ORIGI (A) (C)	ORGA IND	ANISM IVIDU	4: JAL	nomos ISOL <i>I</i>	ATĒ:	SAS			
20	((xi)	S	SEQUE	ENCE	DES	CRIP	rion:	: SEÇ) ID	NO:4	17:	
20	AAT GAAAC CTAAG GACCC ACCC CT	CC TAC AT TGC TG ATT AA GGT CA TTG TT CGG TC TGC	CCA CTG AAT TCA AGG	AAC CAC GTC GCC GTC	TCT GCA AGT CCG GTT	TCC CCT AGG AAC GAC	ATA GGT TGC CTC TAC	GTC TGC TGG GGA TTA	TAC GTG GTC GCG GCG	GAG CCC CAA GTC GGA	GCT TGT ATC ACG GGG	GAT GTC ACC GCT GCT	39 78 117 156 195 234
25	GCA GT CGC CA TAC AC ATG AT GCC CA ATT GC TAC TT	TG TTC AG CAT BC GGC TG ATG AG GTG	TTG ACT CAT AAT CTA GGC TCA	GTA ACG ATC TGG CGG CAC GCG	GGC GTG ACC TCA ATT TGG GCT	CAA CAG GGC CCT CCC GGG AAC	ATG GAC CAC ACG CAA GTC TGG	TTC TGC CGA ACA GTG TTG GCT	ACC AAC ATG GCC GTC TTC AAG	TAT TGT GCA TTG ATT GCC	AGG TCC TGG GTG GAC GTC	CCT ATT GAC ATG ATC GCA	273 312 351 390 429 468 507 546 576
30													

SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid

INFORMATION FOR SEQ ID NO:48:

35

(2)

(i)

0			
		(C) STRANDEDNESS: single (D) TOPOLOGY linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA6	
5	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:48:	
10	AAT GAT TGC COGAC CTG ATC CTG AAG GAT AACCCC ACA CTA TCCCT CTT CGG ACCCCT CTG TGC TCCCC CAG CAT GCC CAG CAT GCC CAG CAT GCC CAG CAT GCC CAG GGC CAG CAT GCC CAG GGC CAG	GG AAT GCC TCT GGG GTG TAT CAT GTT ACC CA AAC TCT TCC ATA GTC TAT GAG GCT GAT CA CAC GCA CCT GGC TGC GTG CCC TGT GTC CAT GTC AGT AGA TGC TGG GTT CAT ATC ACC CA GCC CCG AGC CTC GGA GCG GTC ACG GCT CG GCC GTT GAT TAC TTG GCG GGA GGC CC GCG TTA TAC GTC GGA GAC GTG TGC GGG CC GTA GGC CAA ATG TTC ACC TAT AGG CCT CT ACG GTA CAG GAC TGC AAC TGC TCC ATT CAT ATC ACT GGC CAC CGG ATG GCA TGG GAC CAT TGG TCA CCC GCG ACA GCC TTG GTG ATG	39 78 117 156 195 234 273 312 351 390
15	GCC CAA ATG CT ATT GCC GGG GG TAC TTC GCG TC	TA CGG TCA CCC GCG ACA GCC TTG GTG ATG TA CGG ATT CCC CAG GTG GTC ATT GAC ATC GC CAC TGG GGG GTC TTG TTC GCC GCT GCA TG GCG GCT AAC TGG GCT AAG GTT GTG CTG TG TTT GCG GGG GTT GAT GCC	429 468 507 546 576
	(2) INFORMATI	ON FOR SEQ ID NO:49:	
20	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 576 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA7	
25	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:49:	
30	AAT GAT TGC CCAAC CTG ATC CTG ATC CTG ATC CTG ATC CCT CTT CGG ACCA CTT CTC CCA CTC CTC CTC CTC CTC CT	AAT GCC TCC GGG GTT TAT CAT GTC ACC GAAC TCT TCC ATA GTC TAT GAG GCT GAC GC CAC GCA CCT GGT TGC GTG CCC TGT GTC TGT GTC AGT AGG TGC TGG GTC CAA ATC ACC CA GCC CCG AAC CTC GGA GCG GTC ACG GCT CC GCG CTA TAC GTC GGG GAC GCG TGC GGG CC GTA TAC GTC GGG GAC GCG TGC GGG CC GTA GAC ATG TTC AGC TAT AGG CCT CT ACG GTG CAG GAC TGC AAC TGT TCC ATT CT ATC ACC GGC CAC CGA ATG GCA TGG GAC CT TGG TCA CCT ACG ACA GCC TTG GTG ATG CT CGG ATT CCC CAG GTG GTC ATC GAC ATC CT CGC CAC TGG GTC TTC GCC GCC GCA	39 78 117 156 195 234 273 312 351 390 429 468 507
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0	TAT TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT GTG CT	rg 546
	GTC TTG TTT CTG TTT GCG GGG GTC GAT GCC	576
	(2) INFORMATION FOR SEQ ID NO:50:	
	(i) SEQUENCE CHARACTERISTICS:	
5	(A) LENGTH: 576 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: Homosapiens (C) INDIVIDUAL ISOLATE: SA13	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	
	GTT CCC TAC CGA AAT GCC TCT GGG GTT TAT CAT GTC AC	CC 39
	AAT GAT TGC CCA AAC TCT TCC ATC GTC TAC GAG GCT GA GAC CTG ATC TTA CAC GCA CCT GGT TGC GTG CCC TGT GT	T 117
	AGG CAG GGT AAT GTC AGT AGG TG¢ TGG GTC CAG ATC ACC CCC ACA CTG TCA GCC CCG AGC CT¢ GGA GCG GTC ACG GC	T 195
15	CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGG GGG GCC GCC CTT TGC TCC GCG TTA TAC GTC GGA GAC GCG TGC GG	
	GCA GTG TTT TTG GTA GGT CAA ATG TTC ACC TAT AGC CC CGC CGG CAT AAT GTT GTG CAG GAC TGC AAC TGT TCC AT	T 312
	TAC AGT GGC CAC ATC ACC GGC CAC CGG ATG GCA TGG GA	AC 390
	ATG ATG ATG AAT TGG TCA CCT ACA ACA GCT TTG GTG ATGCC CAG TTG TTA CGG ATT CCC CAG GTG GTC ATT GAC AT	C 468
20	ATT GCC GGG GCC CAC TGG GGG GTC TTG TTC GCC GCC GCT TAC TAC GCG TCG GCG GCT AAC TGG GCC AAG GTT GTG CT	CA 507 CG 546
	GTC CTG TTT CTG TTT GCG GGG GTC GAT GCC	576
	(2) INFORMATION FOR SEQ ID NO:51:	
25	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 576 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: HK2	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
	CTT ACC TAC GGC AAC TCC AGT GGG CTA TAC CAT CTC AC	A 39
	AAT GAT TGC CCC AAC TCC AGC ATC GTG CTG GAG GCG GA GCT ATG ATC TTG CAT TTG CCT GGA TGC TTG CCT TGT GT	G 117
35	AGG GTC GAT GAT CGG TCC ACC TGT TGG CAT GCT GTG AC	CC 156
	372577_1	

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CCC ACC CTG GCC ATA CCA AAT GCT TCC ACG CCC GCA ACG
                                                                 195
      GGA TTC CGC AGG CAT GTG GAT CTT CTT GCG GGC GCC GCA
                                                                 234
      GTG GTT TGC TCA TCC CTG TAC ATC GGG GAC CTG TGT GGC
                                                                 273
      TCT CTC TTT TTG GCG GGA CAA CTA TTC ACC TTT CAG CCC
                                                                 312
      CGC CGT CAT TGG ACT GTG CAA GAC TGC AAC TGC TCC ATC
                                                                 351
      TAT ACA GGC CAC GTC ACC GGC CAC AGG ATG GCT TGG GAC
                                                                 390
      ATG ATG AAC TGG TCA CCC ACA ACC ACT CTG GTC CTA
                                                                 429
 5
      TCT AGC ATC TTG AGG GTA CCT GAG ATT
                                          TGT GCG AGT GTG
                                                                 468
             GGT GGC CAT
                          TGG GGG ATA CTA CTA GCC GTT GCC
                                                                 507
      TAC TTT GGC ATG GCT GGC AAC TGG CTA AAA GTT CTG GCT
                                                                 546
      GTT CTG TTC CTA TTT GCA GGG GTT GAA GCA
                                                                 576
      (2)
           INFORMATION FOR SEQ ID NO:52:
10
           (i)
                     SEQUENCE CHARACTERISTICS:
                      (A)
                          LENGTH:
                                   192 ģmino acids
                      (B)
                          TYPE:
                                  amino acid
                      (C)
                          STRANDEDNESS: unknown
                      (D)
                          TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
15
                      (A)
                          ORGANISM:
                                    homosapiens
                          INDIVIDUAL ISOLATE:
                     (C)
           (xi)
                     SEQUENCE DESCRIPTION: SEO ID NO:52:
      Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
      Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
20
                                                                 30
     His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Val Ser
      Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly
                       50
                                                                 60
     Lys Leu Pro Thr Ala Gln Leu Arg Arg His Ile Asp Leu Leu Val
                                                                 75
25
     Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
                       80
                                            85
                                                                 90
     Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arq
                                           100
                                                                105
     Arg His Trp Thr Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly
                      110
                                           115
                                                                120
     His Ile Thr Gly His Arg Met /Ala Trp Asp Met Met Asn Trp
                      125
                                           130
                                                                135
30
     Ser Pro Thr Thr Ala Leu Val/Val Ala Gln Leu Leu Arg Ile Pro
                      140
                                           145
                                                                150
     Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
                      155
                                           160
     Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
                      170
                                           175
                                                                180
35
```

Leu Val Val Leu Leu Phe Ala Gly Val Asp Ala 185 190

```
(2) INFORMATION FOR SEQ ID NO:53
```

```
(i) SEQUENCE CHARACTER STICS:
```

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: DK9

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr \$\psi lu Ala Ala Asp Ala Ile Leu 20 25 30 15 His Ser Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser Lys Cys Trp Val Ala Val Ala Pro Thr Val Ala Thr Arg Asp Gly 50 55 Lys Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys 85 20 Gly Ser Val Phe Leu Val Gly Glr Leu Phe Thr Phe Ser Pro Arg 100 105 Arg His Trp Thr Thr Gln Asp Cy\$ Asn Cys Ser Ile Tyr Pro Gly 110 115 120 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp 125 130 135 Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro 25 140 145 150 Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu 155 160 Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val 170 175 180 Val Val Leu Leu Phe Thr Gly Val Asp Ala 185 190

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown

35

30

```
(D)
                          TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                      (A)
                          ORGANISM:
                                      homosapiens
                     (C)
                           INDIVIDUAL
                                      ISOLATE:
                                                DR1
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:54:
 5
     His Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
     Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
                       20
                                            25
     His Ala Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
                       35
10
     Arg Cys Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly
     Lys Leu Pro Thr Thr Gln Leu Ard Arg His Ile Asp Leu Leu Val
                                                                 75
     Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
                       80
                                            85
                                                                 90
     Gly Ser Val Phe Leu Val Gly Glh Leu Phe Thr Phe Ser Pro Arg
                       95
                                           100
                                                                105
15
     Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
                      110
                                           115
                                                                120
     His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                      125
                                           130
                                                                135
     Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
                                           145
     Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
                      155
20
                                           160
     Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
                      170
                                           175
     Val Val Leu Leu Phe Ala Gly Val Asp Ala
                      185
      (2)
           INFORMATION FOR SEQ ID NO:55:
25
           (i)
                     SEQUENCE CHARACTERISTICS:
                     (A)
                          LENGTH:
                                   192 amino acids
                     (B)
                          TYPE:
                                  amino acid
                     (C)
                          STRANDEDNESS:
                     (D)
                          TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                     (A)
                          ORGANISM:
                                     homosapiens
30
                     (C)
                          INDIVIDUAL ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:55:
     His Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
```

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Thr Ser Arg Cys Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly 50 55 60 Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val 65 70 75 5 Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys 80 85 Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg 95 100 105 His His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly 110 115 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp 10 125 130 135 Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arq Ile Pro 145 150 Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu 155 160 Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val 170 175 Leu Val Val Leu Leu Phe Ala \$19 Val Asp Ala 15 185

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amind acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ‡SOLATE: S1

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

35

30

```
Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
                                         100
    Arg Leu Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
                                                             120
    His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                                         130
                                                             135
    Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
                                         145
5
    Gln Ala Ile Leu Asp Met Ile Ala $ly Ala His Trp Gly Val Leu
                    155
                                         160
    Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
                    170
                                         175
    Leu Val Val Leu Leu Phe Ala Gly Val Asp Ala
                    185
                                         190
```

10 (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE
 - (A) ORGANISM: | homosapiens
 - (C) INDIVIDUAL ISOLATE: S18
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:57:
- Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp 20 Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Thr Ile Leu 25 His Ser Pro Gly Cys Val Pro ¢ys Val Arg Glu Gly Asn Ala Ser 40 35 45 Arg Cys Trp Val Pro Val Ala Pro Thr Val Ala Thr Arg Asp Gly 50 25 Lys Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val 65 70 75 Gly Ser Ala Thr Leu Cys Ser/Ala Leu Tyr Val Gly Asp Leu Cys 80 85 90 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg 105 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly 110 115 120 30 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 Ser Pro Thr Thr Ala Leu Val Ile Ala Gln Leu Leu Arg Val Pro 140 145 150 Gln Ala Val Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu 155 160

35

```
- 116 -
      Ala Gly Ile Ala Tyr Phe Ser Met Ala Gly Asn Trp Ala Lys Val
                                           175
     Leu Leu Val Leu Leu Phe Ala Gly/Val Asp Ala
                      185
                                           190
      (2)
           INFORMATION FOR SEQ ID NO:58:
 5
           (i)
                     SEQUENCE CHARACTER STICS:
                      (A)
                          LENGTH:
                                    192 amino acids
                                  amino/acid
                      (B)
                           TYPE:
                      (C)
                           STRANDEDNESS
                                          unknown
                           TOPOLOGY:
                                      u/nknown
                      (D)
           (vi)
                     ORIGINAL SOURCE:
                                      homosapiens
10
                      (A)
                          ORGANISM:
                     (C)
                           INDIVIDUAL / ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:58:
     Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp
      Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Ala Ile Leu
15
                       20
     His Ser Pro Gly Cys Val Pro ¢ys Val Arg Glu Asp Gly Ala Pro
     Lys Cys Trp Val Ala Val Ala Pro Thr Val Ala Thr Arq Asp Gly
                       50
                                            55
     Lys Leu Pro Ala Thr Gln Leu/Arg Arg His Ile Asp Leu Leu Val
     Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
20
                                                                 90
     Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
                                                                105
                       95
                                           100
     Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
                                           115
                                                                120
     His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                      125
                                           130
                                                                135
25
     Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
                      140
                                           145
     Gln Ala Val Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
                      155
                                           160
     Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
                      170
                                           175
     Leu Ile Val Leu Leu Phe Ser Gly Val Asp Ala
                      185
30
      (2)
           INFORMATION FOR SEO ID NO:59:
         (i)
                     SEQUENCE CHARACTERISTICS:
                      (A)
                          LENGTH:
                                    192 amino acids
                          TYPE:
                     (B)
                                  amino acid
35
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```
(C)
                           STRANDEDNESS:
                                           unknown
                      (D)
                           TOPOLOGY:
                                     unknown
           (vi)
                     ORIGINAL SOURCE:
                           ORGANISM:
                      (A)
                                      homosapiens
                      (C)
                           INDIVIDUAL ISOLATE:
                                                 US11
 5
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:59:
      Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
      Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
                        20
                                             25
      His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
                        35
10
      Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly
      Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
                        65
                                                                  75
      Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
                        80
                                             85
                                                                  90
      Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
15
                        95
                                            100
                                                                 105
      Arg His Trp Thr Thr Gln Gl∳ Cys Asn Cys Ser Ile Tyr Pro Gly
                       110
                                            115
                                                                 120
      His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
                      125
                                            130
      Ser Pro Thr Ala Ala Leu Val Val Ala Gln Leu Leu Arq Ile Pro
                                            145
                                                                 150
      Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
20
                       155
                                                                 165
      Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
                      170
                                                                 180
      Leu Val Val Leu Leu Phe Ala Gly Val Asp Ala
                      185
25
      (2)
           INFORMATION FOR SEQ ID NO:60:
           (i)
                     SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH:
                                    192 amino acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                           unknown
                      (D)
                           TOPOLOGY:
                                      unknown
30
           (vi)
                     ORIGINAL SOURCE:
                      (A)
                           ORGANISM:
                                      homosapiens
                      (C)
                           INDIVIDUAL ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:60:
35
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```
Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
     Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
                                                                 30
     His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn Ser Ser
                                                                 45
                                            40
     Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Gly
                                            55
                                                                 60
5
     Asn Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val
                       65
                                            70
                                                                 75
     Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
                       80
                                            85
     Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Leu Ser Pro Arg
                       95
                                           100
     Arg His Glu Thr Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
10
                      110
                                           115
                                                                120
     His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
                                           130
                                                                135
     Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
                      140
                                           145
     Gln Ala Val Met Asp Met Val Ala Ġly Ala His Trp Gly Val Leu
                      155
                                           160
                                                                165
     Ala Gly Leu Ala Tyr Tyr Ser Met Nal Gly Asn Trp Ala Lys Val
15
                      170
                                           175
     Leu Ile Val Met Leu Leu Phe Ala/Gly Val Asp Gly
                      185
                                           190
```

(2) INFORMATION FOR SEQ ID NO 61:

- 20 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1/92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: D3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

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```
- 119 -
      Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
      Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
                                                                105
      Arg His Glu Thr Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
                      110
                                           115
                                                                120
      His Val Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                                           130
 5
      Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
                      140
                                           145
                                                                150
      Gln Ala Val Val Asp Met Val Ala/Gly Ala His Trp Gly Val Leu
                      155
                                           160
      Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
                      170
                                           175
      Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
10
                      185
      (2)
           INFORMATION FOR SEQ ID NO:62:
           (i)
                     SEQUENCE CHARACTERISTICS:
                     (A)
                          LENGTH: |192 amino acids
                     (B)
                          TYPE:
                                  amino acid
15
                      (C)
                          STRANDEDNESS:
                                          unknown
                      (D)
                          TOPOLOGY:
                                     unknown
           (vi)
                     ORIGINAL SOURCE:
                     (A)
                          ORGANISM:
                                      homosapiens
                     (C)
                           INDIVIDUAL ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:62:
20
      Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
      Cys Ser Asn Ser Ser Ile Vall Tyr Glu Ala Val Asp Val Ile Met
                       20
                                            25
     His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn His Ser
25
     Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
                                            55
      Ser Ile Pro Thr Thr Tile Arg Arg His Val Asp Leu Leu Val
                       65
                                            70
      Gly Ala Ala Ala Phe Cys $er Ala Met Tyr Val Gly Asp Leu Cys
                                            85
                                                                 90
     Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
                                           100
                                                                105
30
     Arg His Glu Thr Ala Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
                      110
                                           115
     His Val Ser Gly His Arg | Met Ala Trp Asp Met Met Asn Trp
                      125
                                           130
                                                                135
      Ser Pro Thr Thr Ala Leu Val Leu Ser Gln Leu Leu Arg Ile Pro
                      140
                                           145
                                                                150
35
```

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Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155
160
165
Ala Gly Leu Ala Tyr Tyr Ser Met Ala Gly Asn Trp Ala Lys Val
170
175
180
Leu Ile Val Leu Leu Phe Ala Gly Val Asp Gly
185
190
```

5 (2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

10

·(vi)

ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: HK3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
- Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp 15 Cys Ser Asn Ser Ser Val Val Tyr Glu Thr Ala Asp Met Ile Met 25 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser 35 40 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Val Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val 20 75 Gly Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys 80 85 90 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg 95 100 105 Arg His Glu Thr Val Gln Asp ¢ys Asn Cys Ser Leu Tyr Pro Gly 110 115 120 25 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 135 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro 140 145 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu 155 160 165 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 170 175 30 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly 185 190
 - (2) INFORMATION FOR SEQ ID NO:64:
 - (i) SEQUENCE CHARACTERISTICS:

```
(A)
                           LENGTH:
                                     192 amilno acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                           unknown
                      (D)
                           TOPOLOGY:
                                      unknown
           (vi)
                      ORIGINAL SOURCE:
                      (A)
                           ORGANISM:
                                      homosapiens
 5
                      (C)
                           INDIVIDUAL ISOLATE:
                                                 HK4
           (xi)
                      SEQUENCE DESCRIPTION: SEQ ID NO:64:
      His Glu Val His Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
      Cys Ser Asn Ser Ser Ile Val Tyr Gļu Ala Ala Asp Met Ile Met
10
      His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
                                                                  45
      Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
                        50
                                             55
                                                                  60
      Ser Ile Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
                        65
                                             70
                                                                  75
      Gly Ala Ala Ala Phe Cys Ser Ala/Met Tyr Val Gly Asp Leu Cys
15
                        80
                                             85
                                                                  90
      Gly Ser Val Phe Leu Val Ser Glm/ Leu Phe Thr Phe Ser Pro Arg
                                            100
                                                                 105
      Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
                       110
                                            115
      His Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                                            130
                                                                 135
      Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arq Leu Pro
20
                                                                 150
      Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
                       155
                                            160
      Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
                       170
                                            175
                                                                 180
      Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
                       185
                                            190
25
      (2)
           INFORMATION FOR SEQ ID NO:65:
           (i)
                      SEQUENCE CHARACTERISTICS:
                                    192 amino acids
                      (A)
                           LENGTH:
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                           unknown
30
                           TOPOLOGY:
                      (D)
                                      unknown
           (vi)
                      ORIGINAL SOURCE:
                           ORGANISM:
                      (A)
                                      homosapiens
                           INDIVIDUAL ISOLATE:
                      (C)
           (xi)
                      SEQUENCE DESCRIPTION: SEQ ID NO:65:
35
```

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp Cys Ser Asn Leu Ser Ile Val Tyr \$lu Thr Thr Asp Met Ile Met 30 25 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser 5 Arg Cys Trp Val Ala Leu Ala Pro Thr Leu Ala Ala Arg Asn Ala 50 55 Ser Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val 70 Gly Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys 85 80 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg 10 100 105 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly 120 His Val Thr Gly His Arg Met Ala! Trp Asp Met Met Met Asn Trp 130 135 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro 140 145 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu 15 155 160 Ala Gly Leu Ala Tyr Tyr Ser Me't Val Gly Asn Trp Ala Lys Val 170 175 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly

(2) INFORMATION FOR SEQ ID NO:66:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY! unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: HK8
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
20 25 30
His Thr Pro Gly Cys Met Pro Cys Val Arg Glu Asn Asn Ser Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Val
50 55 60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val

35

25

Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arq 95 100 105 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly 110 115 120 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 5 125 130 135 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro 140 145 150 Gln Ala Ile Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu 155 160 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 170 175 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly 10 185 190

(2) INFORMATION FOR SEQ ID NO 67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:

140

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: IND5
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Trr Glu Ala Ala Asp Met Ile Met 25 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ser Ser 25 Arg Cys Trp Val Ala Leu Thr Pto Thr Leu Ala Ala Arg Asn Ala 50 55 Ser Val Ser Thr Thr Ile Atg His His Val Asp Leu Leu Val 75 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys 90 Gly Ser Val Phe Leu Val Ser Gin Leu Phe Thr Phe Ser Pro Arg 30 95 100 105 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly 115 120 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 135

Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro

145

150

35

Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Ile Leu 160 Ala Gly Leu Ala Tyr Tyr Ser Met | Val Gly Asn Trp Ala Lys Val 170 175 180 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly 5 (2) INFORMATION FOR SEQ ID NO:68: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 192 amino acids (B) TYPE: amind acid (C) STRANDEDNESS: unknown 10 (D) TOPOLOGY: unknown (vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: IND8 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68: 15 Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met 2.0 25 His Thr Pro Gly Cys Val Pro Cy\$ Val Arg Glu Gly Asn Phe Ser Ser Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala 20 60 Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val 65 70 75 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys 85 90 Gly Ser Val Phe Leu Val Ser Glin Leu Phe Thr Phe Ser Pro Arg 95 100 105 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly 25 110 115 120 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro 140 145 150 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Ile Leu 155 160 165 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 30

175

190

180

(2) INFORMATION FOR SEQ ID No. 69:

170

185

Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly

```
(i)
                      SEQUENCE CHARACTERISTICS:
                                    192 amino acids
                      (A)
                           LENGTH:
                      (B)
                           TYPE:
                                  amind acid
                      (C)
                           STRANDEDNESS:
                                           unknown
                      (D)
                           TOPOLOGY:
                                      unknown
           (vi)
                      ORIGINAL SOURCE:
 5
                      (A)
                           ORGANISM:
                                      homosapiens
                           INDIVIDUAL | SOLATE:
                      (C)
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:69:
      Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
      Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
10
      His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
      Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser
                                             55
      Ser Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val
                        65
                                             70
15
      Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
                        80
                                             85
      Gly Ser Val Leu Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
                        95
                                            100
                                                                 105
      Arg His Trp Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
                       110
                                            115
                                                                 120
      His Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                                            130
                                                                 135
20
      Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
                       140
                                            145
                                                                 150
      Gln Ala Ile Leu Asp Val Val Ala Gly Ala His Trp Gly Val Leu
                       155
                                            160
      Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
                       170
                                            175
      Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
25
                       185
                                            190
           INFORMATION FOR SEQ ID NO: 70:
           (i)
                      SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH:
                                    192 amino acids
                      (B)
                           TYPE:
                                  aminb acid
30
                      (C)
                           STRANDEDNESS:
                                           unknown
                      (D)
                           TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                           ORGANISM:
                                      homosapiens
                      (A)
                      (C)
                           INDIVIDUAL ISOLATE:
35
```

```
(xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:70:
      Tyr Glu Val Arg Asn Val Ser Gly Ala Tyr His Val Thr Asn Asp
                                                                  15
      Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Val Ile Met
      His Thr Pro Gly Cys Val Pro Cys Val Gln Glu Gly Asn Ser Ser
                                                                  45
      Gln Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
      Thr Val Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
                        65
                                            70
      Gly Ala Ala Val Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
                                             85
      Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Ile Ser Pro Arg
10
      Arg His Glu Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Pro Gly
                       110
                                           115
                                                                 120
      His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
                      125
                                           130
      Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
                      140
                                           145
                                                                 150
15
      Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
                      155
                                           160
      Ala Gly Leu Ala Tyr Tyr Ser Met | Val Gly Asn Trp Ala Lys Val
                      170
                                           175
                                                                 180
      Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
20
      (2)
           INFORMATION FOR SEQ ID NO:71:
           (i)
                     SEQUENCE CHARACTERISTICS:
                      (A)
                          LENGTH:
                                    192 amino acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                          unknown
                           TOPOLOGY:
                      (D)
                                      unknown
25
           (vi)
                     ORIGINAL SOURCE
                      (A)
                           ORGANISM:
                                      homosapiens
                      (C)
                           INDIVIDUAL | ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:71:
      Tyr Glu Val Arg Asn Val Ser Gly Ala Tyr His Val Thr Asn Asp
30
      Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Val Asp Val Ile Leu
     His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
                                            40
     Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser
                                                                 60
35
     372577_1
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0								İ							
	Ser	Val	Pro	Thr	Thr 65	Thr	Ile	Arg	Arg	His 70	Val	Asp	Leu	Leu	Val 75
	Gly	Ala	Ala	Ala	Phe 80	Cys	Ser	Ala	Met	Tyr 85	Val	Gly	Asp	Leu	Cys 90
	Gly	Ser	Val	Phe	Leu 95	Val	Ser	Glh	Leu	Phe 100	Thr	Phe	Ser	Pro	Arg 105
5	Arg	His	Glu	Thr	Val 110	Gln	Asp	Cys	Asn	Cys 115	Ser	Ile	Tyr	Pro	Gly 120
	His	Val	Thr	Gly	His 125	Arg	Met	Ala	Trp	Asp 130	Met	Met	Met	Asn	Trp 135
	Ser	Pro	Thr	Ala	Ala 140	Leu	Val	Val	Ser	Gln 145	Leu	Leu	Arg	Ile	Pro 150
	Gln	Ala	Val	Val	Asp 155	Met	Val	Ala	Gly	Ala 160	His	Trp	Gly	Val	
10	Ala	Gly	Leu	Ala	Tyr 170	Tyr	Ser	Met	Val	Gly 175	Asn	Trp	Ala	Lys	
	Leu	Ile	Val	Met	Leu 185	Leu	Phe	Ala	Gly		Asp	Gly			
	(2) INFORMATION FOR SEQ ID NO:72:														
15		(i))		SEQUI (A)	LENC	GTH:	19:	ERIST	ino a		5			

(B) TYPE: amin pacid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp 15 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met 20 25 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser 35 40 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser 50 55 60 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val 65 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys 80 85 90 30 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arq 95 100 105 Arg Tyr Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly 110 115 Arg Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp 125 130 135

35

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Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro 140

Gln Ala Ile Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu 155

Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 170

Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly 190
```

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met 20 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Ala Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Thr 20 55 Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val 65 70 75 Gly Ala Ala Ala Phe Cys Ser Val Met Tyr Val Gly Asp Leu Cys 85 80 90 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg 95 100 105 25 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly 110 115 120 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 135 Ser Pro Thr Ala Ala Leu Val | Val Ser Gln Leu Leu Arg Ile Pro 140 145 150 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu 155 160 165 30 Ala Gly Leu Ala Tyr Tyr Ser/Met Val Gly Asn Trp Ala Lys Val 170 175 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly 185 190

(2) INFORMATION FOR SEQ ID NO:74:

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(i)
                      SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH:
                                    192 amino acids
                      (B)
                           TYPE:
                                  amlino acid
                      (C)
                           STRANDEDNESS:
                                           unknown
                           TOPOLOGY:
                      (D)
                                      unknown
 5
           (vi)
                      ORIGINAL SOURCE:
                      (A)
                           ORGANISM:
                                      homosapiens
                      (C)
                           INDIVIDUAL
                                      ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:74:
      Tyr Glu Val Arg Asn Val Ser Gly Val Tyr Tyr Val Thr Asn Asp
10
      Cys Ser Asn Ser Ser Ile Val Tyt Glu Thr Ala Asp Met Ile Met
     His Thr Pro Gly Cys Val Pro Cy$ Val Arg Glu Ser Asn Ser Ser
                        35
      Arg Cys Trp Val Ala Leu Thr Prф Thr Leu Ala Ala Arg Asn Ala
      Ser Val Pro Thr Lys Thr Ile Ard Arg His Val Asp Leu Leu Val
15
     Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
                        80
                                             85
     Gly Ser Val Phe Leu Val Ser Glh Leu Phe Thr Phe Ser Pro Arg
                        95
                                            100
     Arg His Glu Thr Val Gln Asp Cy$ Asn Cys Ser Ile Tyr Pro Gly
                                            115
                                                                 120
     His Val Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp
20
                                            130
                                                                 135
      Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
                       140
                                            145
     Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
                       155
                                            160
     Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
                       170
                                            175
25
     Leu Ile Val Leu Leu Phe Ala Gly Val Asp Gly
                       185
                                            190
      (2)
           INFORMATION FOR SEQ ID NO:75:
           (i)
                      SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH:
                                    192 amino acids
30
                      (B)
                           TYPE:
                                  amilno acid
                      (C)
                           STRANDEDNESS:
                                          unknown
                      (D)
                           TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                      (A)
                           ORGANISM:
                                      homosapiens
                      (C)
                           INDIVIDUAL ISOLATE:
35
```

35

372577_1

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SEQUENCE DESCRIPTION: SEQ ID NO:75:
           (xi)
     Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp
     Cys Ser Asn Ser Ser Ile Val Phe Glu Ala Ala Asp Leu Ile Met
                       20
 5
     His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ser Ser
     Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Thr
                       50
                                            55
     Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
     Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
                                                                 90
10
     Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
                       95
                                           100
                                                                105
     Arg His Glu Thr Leu Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
                      110
                                           115
                                                                120
     His Leu Ser Gly His Arg Met Ala
                                       Trp Asp Met Met Met Asn Trp
                      125
                                           130
                                                                135
     Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
15
                      140
                                           145
                                                                150
     Gln Ala Val Met Asp Met Val Thr Gly Ala His Trp Gly Val Leu
                                           160
                      155
     Ala Gly Leu Ala Tyr Tyr Ser Met Ala Gly Asn Trp Ala Lys Val
                                           175
     Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
                                           190
                      185
20
           INFORMATION FOR SEQ ID NO: 76:
      (2)
           (i)
                     SEQUENCE CHARACTERISTICS:
                          LENGTH:
                                    192 amino acids
                     (A)
                     (B)
                          TYPE:
                                  amiho acid
                      (C)
                          STRANDEDNESS:
                                          unknown
25
                          TOPOLOGY:
                      (D)
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                     (A)
                          ORGANISM:
                                      homosapiens
                     (C)
                          INDIVIDUAL ISOLATE:
                     SEQUENCE DESCRIPTION: SEQ ID NO:76:
           (xi)
30
     Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp
     Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
                                            25
     His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
```

130 -

131 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val 65 75 Gly Ala Ala Thr Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys 90 Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Phe Ser Pro Arg 95 100 105 5 Gln His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly 110 115 120 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arq Ile Pro 140 145 Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu 10 165 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 170 175 Leu Ile Val Leu Leu Phe Ala Gly Val Asp Gly (2) INFORMATION FOR SEQ ID NO:77: 15 (i)SEQUENCE CHARACTERISTICS: (A) LENGTH: 192 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown (vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens 20 (C) INDIVIDUAL ISOLATE: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77: Ala Gln Val Arg Asn Thr Ser Arg Gly Tyr Met Val Thr Asn Asp Cys Ser Asn Glu Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu 25 25 His Val Pro Gly Cys Ile Pro Cys Glu Arg Leu Gly Asn Thr Ser Arg Cys Trp Ile Pro Val Thr Pro Asn Val Ala Val Arg Gln Pro Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val 75 70 Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys 30 90 Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Val Ser Pro Arg 95 100 105 Arg His Trp Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly 110 115 120 Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 35

Ser Pro Thr Ala Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro
140 145 150

Glu Val Ile Ile Asp Ile Ile Gly Gly Ala His Trp Gly Val Met
155 160 165

Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
170 175 180

Ile Val Ile Leu Leu Leu Ala Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTÉRISTICS:
 - (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: T
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ala Gln Val Lys Asn Thr Thr Asn Ser Tyr Met Val Thr Asn Asp 10 Cys Ser Asn Asp Ser Ile Thr Tro Gln Leu Gln Ala Ala Val Leu His Val Pro Gly Cys Val Pro Cys Glu Lys Thr Gly Asn Thr Ser 35 45 20 Arg Cys Trp Ile Pro Val Ser Pro Asn Val Ala Val Arg Gln Pro 50 55 60 Gly Ala Leu Thr Gln Gly Leu Ard Thr His Ile Asp Met Val Val 75 Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys 80 85 90 Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Val Ser Pro Gln 25 100 105 His His Trp Phe Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly 110 115 Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 135 Ser Pro Thr Ala Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro 145 150 Glu Val Ile Leu Asp Ile Val Ser Gly Ala His Trp Gly Val Met 30 155 160 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val 170 175 180

Val Val Ile Leu Leu Leu Ala Ala Gly Val Asp Ala

185

190

35

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(2)
           INFORMATION FOR SEQ ID NO: 79:
           (i)
                      SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH:
                                    192 amino acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                          unknown
                      (D)
                           TOPOLOGY:
                                      uhknown
 5
           (vi)
                      ORIGINAL SOURCE:
                      (A)
                           ORGANISM:
                                      homosapiens
                      (C)
                           INDIVIDUAL ISOLATE:
           (xi)
                      SEQUENCE DESCRIPTION: SEQ ID NO:79:
     Ala Glu Val Lys Asn Thr Ser Thr Ser Tyr Met Val Thr Asn Asp
10
      Cys Ser Asn Asp Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu
     His Val Pro Gly Cys Val Pro Cys Glu Arg Val Gly Asn Ala Ser
      Arg Cys Trp Ile Pro Val Ser Pro Asn Val Ala Val Gln Arg Pro
                        50
15
      Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val
                        65
                                             70
                                                                  75
     Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
                                             85
                        80
      Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Ile Ser Pro Gln
                                            100
                                                                 105
     His His Trp Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
                                            115
                                                                 120
20
      Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                       125
                                            130
                                                                 135
      Ser Pro Thr Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro
                       140
                                            145
                                                                 150
     Glu Val Ile Ile Asp Ile Ile Ser Gly Ala His Trp Gly Val Met
                      155
                                            160
     Phe Gly Leu Ala Tyr Phe Ser Met |Gln Gly Ala Trp Ala Lys Val
25
                       170
                                            175
                                                                 180
     Val Val Ile Leu Leu Thr Ala Gly Val Asp Ala
                       185
                                            190
      (2)
           INFORMATION FOR SEQ ID NO:80:
                     SEQUENCE CHARACTERISTICS:
           (i)
30
                      (A)
                           LENGTH:
                                    192 amino acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                          unknown
                      (D)
                           TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                      (A)
                           ORGANISM:
                                      homosapiens
35
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(C)
                           INDIVIDUAL ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:80:
     Val Gln Val Lys Asn Thr Ser Thr Ser Tyr Met Val Thr Asn Asp
                                             10
     Cys Ser Asn Asp Ser Ile Thr Trp Gln Leu Glu Ala Ala Val Leu
 5
                                             25
     His Val Pro Gly Cys Val Pro Cys Glu Lys Val Gly Asn Thr Ser
                        35
                                             40
     Arg Cys Trp Ile Pro Val Ser Pro Asn Val Ala Val Gln Arg Pro
     Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val
                                                                  75
     Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Phe Cys
10
                       80
                                             85
                                                                  90
     Gly Gly Met Met Leu Ala Ala Gln Met Phe Ile Val Ser Pro Arg
                       95
                                           100
                                                                 105
     His His Ser Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
                      110
                                           115
                                                                 120
     Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                      125
                                           130
                                                                 135
15
     Ser Pro Thr Ala Thr Leu Ile Leu Ala Tyr Val Met Arg Val Pro
                      140
                                           145
                                                                 150
     Glu Val Ile Ile Asp Ile Ile Ser Gly Ala His Trp Gly Val Leu
                      155
                                           160
                                                                 165
     Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
                      170
                                           175
     Val Val Ile Leu Leu Leu Ala Ala Gly Val Asp Ala
                      185
20
      (2)
           INFORMATION FOR SEQ ID NO:81:
           (i)
                     SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH:
                                    192 amino acids
                      (B)
                           TYPE:
                                  amilno acid
25
                      (C)
                           STRANDEDNESS:
                                          unknown
                      (D)
                           TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                      (A)
                           ORGANISM:
                                      homosapiens
                      (C)
                           INDIVIDUAL ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:81:
30
     Val Glu Val Arg Asn Ile Ser Ser Ser Tyr Tyr Ala Thr Asn Asp
     Cys Ser Asn Asn Ser Ile Thr Trp Gln Leu Thr Asp Ala Val Leu
     His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu
                                            40
                                                                  45
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J								1							
	Arg	Cys	Trp	Ile	Gln 50	Val	Thr	Pro	Asn	Val 55	Ala	Val	Lys	His	Arg 60
	Gly	Ala	Leu	Thr	His 65	Asn	Leu	Arg	Thr	His 70	Val	Asp	Val	Ile	Val 75
	Met	Ala	Ala	Thr	Val 80	Cys	Ser	Ala	Leu	Tyr 85	Val	Gly	Asp	Val	Cys 90
5	Gly	Ala	Val	Met	Ile 95	Val	Ser	Gln	Ala	Leu 100	Ile	Ile	Ser	Pro	Glu 105
	Arg	His	Asn	Phe	Thr 110	Gln	Glu	Cys	Asn	Cys 115	Ser	Ile	Tyr	Gln	Gly 120
	His	Ile	Thr	Gly	His 125	Arg	Met	Ala	Trp	Asp 130	Met	Met	Leu	Asn	Trp 135
	Ser	Pro	Thr	Leu	Thr 140	Met	Ile	Leu	Ala	Tyr 145	Ala	Ala	Arg	Val	Pro 150
10	Glu	Leu	Ala	Leu	Gln 155	Val	Val	Phe	Gly	Gly 160	His	Trp	Gly	Val	Val 165
	Phe	Gly	Leu	Ala	Tyr 170	Phe	Ser	Met	Gln	Gly 175	Ala	Trp	Ala	Lys	Val 180
	Ile	Ala	Ile	Leu	Leu 185	Leu	Val	Ala	Gly	Val 190	Asp	Ala			
									1						

15 (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: DK11
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Val Glu Val Arg Asn Thr Ser Ser Ser Tyr Tyr Ala Thr Asn Asp 25 10 Cys Ser Asn Asn Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu His Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg 55 60 Gly Ala Leu Thr His Asn Leu Arg Ala His Ile Asp Met Ile Val 30 65 70 75 Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys 80 85 90 Gly Ala Val Met Ile Val Ser Gln Ala Phe Ile Val Ser Pro Glu 95 100 His His His Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly 110 115 120

35

His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp 125 130 Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro 140 145 Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val 155 160 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val 5 170 175 Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala 185 190

(2) INFORMATION FOR SEQ ID NO:83:

- 10 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: SW3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Val Glu Val Arg Asn Ile Ser Ser Ser Tyr Tyr Ala Thr Asn Asp Cys Ser Asn Ser Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu 30 20 His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu 40 45 His Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg 55 60 Gly Ala Leu Thr His Asn Leu Arg Ala His Val Asp Met Ile Val 65 70 75 Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Met Cys 25 80 85 Gly Ala Val Met Ile Val Ser Gln Ala Phe Ile Ile Ser Pro Glu 95 100 Arg His Asn Phe Thr Gln Glu dys Asn Cys Ser Ile Tyr Gln Gly 110 115 Arg Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp 130 135 Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro 30 140 145 Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val 155 160 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val 170 175 180 Ile Ala Ile Leu Leu Val Ala Gly Val Asp Ala 185 190

35

```
(2)
           INFORMATION FOR SEQ ID NO:84:
           (i)
                      SEQUENCE CHARACTERISTICS:
                           LENGTH:
                                   192 amino acids
                      (A)
                      (B)
                           TYPE:
                                  amino acid
 5
                           STRANDEDNESS:
                      (C)
                                           unknown
                           TOPOLOGY:
                      (D)
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                      (A)
                           ORGANISM:
                                      homosapiens
                      (C)
                           INDIVIDUAL ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:84:
10
     Val Glu Val Arg Asn Thr Ser the Ser Tyr Tyr Ala Thr Asn Asp
      Cys Ser Asn Asn Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu
                        20
     His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu
15
     Arg Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg
                        50
                                             55
      Gly Ala Leu Thr His Asn Leu Arg Thr His Val Asp Val Ile Val
                        65
                                             70
     Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
                                             85
                                                                  90
      Gly Ala Val Met Ile Ala Ser $\oldsymbol{\psi}$ln Ala Phe Ile Ile Ser Pro Glu
                                                                 105
20
      Arg His Asn Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
                       110
                                            115
                                                                 120
     His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
                       125
                                            130
                                                                 135
      Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
                       140
                                            145
      Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val
25
                       155
                                            160
      Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
                       170
                                            175
      Ile Ala Ile Leu Leu Val Ala Gly Val Asp Ala
                       185
                                            190
      (2)
           INFORMATION FOR SEQ ID NO:85:
30
           (i)
                      SEQUENCE CHARACTERISTICS:
                           LENGTH:
                                    192 amino acids
                      (A)
                           TYPE:
                                  amino acid
                      (B)
                      (C)
                           STRAND#DNESS:
```

unknown

unknown

35

(D)

TOPOLOGY:

```
(vi)
                     ORIGINAL SOURCE:
                          ORGANISM: homosapiens
                     (A)
                     (C)
                          INDIVIDUAL ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:85:
     Val Glu Val Lys Asp Thr Gly Asp Ser Tyr Met Pro Thr Asn Asp
 5
      Cys Ser Asn Ser Ser Ile Val Trp Gln Leu Glu Gly Ala Val Leu
                       20
                                            25
     His Thr Pro Gly Cys Val Pro Cy's Glu Arg Thr Ala Asn Val Ser
     Arg Cys Trp Val Pro Val Ala Pro Asn Leu Ala Ile Ser Gln Pro
     Gly Ala Leu Thr Lys Gly Leu Arg Ala His Ile Asp Ile Ile Val
10
                                                                 75
                                            70
     Met Ser Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
                       80
                                            85
                                                                 90
      Gly Ala Leu Met Leu Ala Ala Gln Val Val Val Ser Pro Gln
                       95
                                           100
                                                                105
     His His Thr Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
                      110
                                           115
                                                                120
15
     Arg Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                      125
                                           130
                                                                135
      Ser Pro Thr Thr Met Leu Leu Ala Tyr Leu Val Arg Ile Pro
                      140
                                           145
     Glu Val Ile Leu Asp Ile Val Thr Gly Gly His Trp Gly Val Met
                      155
                                           160
                                                                165
      Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ser Trp Ala Lys Val
                      170
                                           175
20
      Ile Val Ile Leu Leu Thr Ala Gly Val Glu Ala
                      185
      (2)
           INFORMATION FOR SEQ ID NO:86:
           (i)
                     SEQUENCE CHARACTERISTICS:
25
                          LENGTH:
                     (A)
                                   192 amino acids
                     (B)
                          TYPE:
                                 amino acid
                     (C)
                          STRANDEDNESS:
                                          unknown
                     (D)
                          TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                     (A)
                          ORGANISM:
                                      homosapiens
                     (C)
                          INDIVIDUAL ISOLATE:
                                                DK12
30
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:86:
     Leu Glu Trp Arg Asn Val Ser Gly Leu Tyr Val Leu Thr Asn Asp
     Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
                       20
```

His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Ser Val Thr Pro Thr Val Ala Val Arg Tyr Val 55 60 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val 65 70 75 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Val Cys 5 80 85 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg 95 100 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly 110 115 120 His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 130 135 Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro 10 140 145 150 Gln Thr Leu Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Met 155 160 Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val 170 175 180 Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala 185 190 15

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: HK10
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Leu Glu Trp Arg Asn Val Ser Gly Leu Tyr Val Leu Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser 40 45 Thr Cys Trp Thr Ser Val Thr Pro Thr Val Ala Val Arg Tyr Val 30 50 Gly Ala Thr Thr Ala Ser Ile Arg| Ser His Val Asp Leu Leu Val 65 70 75 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys 80 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg 100 105

35

20

Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly 110 115 120 His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 135 Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro 140 145 150 Gln Thr Leu Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Leu 5 155 160 Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val 170 175 Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala 185

(2) INFORMATION FOR SEQ ID NO:88:

10 (i) SEQUENCE CHARAGTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu 20 30 His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser 40 Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val 50 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val 75 25 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys 80 85 90 Gly Ala Val Phe Leu Val Gly Glh Ala Phe Thr Phe Arg Pro Arg 105 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly 120 His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 135 30 Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arq Leu Pro 140 145 Gln Thr Val Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Leu 155 160 Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val 170 175 180

35

```
Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala
                       185
      (2)
           INFORMATION FOR SEQ ID NO:89:
           (i)
                     SEQUENCE CHARACTERISTICS:
                           LENGTH:
                                    192 amino acids
                      (A)
 5
                      (B)
                           TYPE:
                                  amino acid
                           STRANDEDNESS:
                      (C)
                                          unknown
                      (D)
                           TOPOLOGY:
                                      lunknown
           (vi)
                     ORIGINAL SOURCE:
                      (A)
                           ORGANISM:
                                      homosapiens
                      (C)
                           INDIVIDUAL | ISOLATE:
10
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:89:
     Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu Thr Asn Asp
     Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
     His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
15
     Met Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
                                             55
     Gly Ala Thr Thr Ala Ser Ile Ard Ser His Val Asp Leu Leu Val
                                             70
     Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
     Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
20
                                            100
                                                                 105
     Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
                       110
                                            115
                                                                 120
     His Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                       125
                                            130
                                                                 135
     Ser Pro Ala Val Gly Met Val Val Ala His Ile Leu Arg Leu Pro
                       140
                                            145
                                                                 150
25
     Gln Thr Leu Phe Asp Ile Leu Ala Gly Ala His Trp Gly Ile Leu
                       155
                                            160
                                                                 165
     Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
                       170
                                            175
                                                                 180
     Ala Ile Val Met Ile Met Phe Ser Gly Val Asp Ala
                       185
30
      (2)
           INFORMATION FOR SEQ ID NO:90:
           (i)
                     SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH:
                                   192 amino acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                          unknown
                      (D)
                           TOPOLOGY:
                                     unknown
35
```

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(vi)
                     ORIGINAL SOURCE
                      (A)
                           ORGANISM:
                                      homosapiens
                      (C)
                           INDIVIDUAL ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:90:
 5
     Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Ile Leu Thr Asn Asp
     Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
                       20
                                             25
     His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
                       35
     Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
10
     Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
                       65
                                                                  75
     Gly Ala Ala Thr Leu Cys Ser Aḷa Leu Tyr Val Gly Asp Met Cys
                                                                  90
     Gly Ala Val Phe Leu Val Gly Gİn Ala Phe Thr Phe Arg Pro Arg
                       95
                                           100
                                                                 105
     Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
15
                      110
                                           115
                                                                 120
     His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                      125
                                           130
     Ser Pro Ala Val Gly Met Val Val Ala His Ile Leu Arg Leu Pro
                      140
                                           145
     Gln Thr Leu Phe Asp Ile Leu Ala Gly Ala His Trp Gly Ile Leu
                      155
                                           .160
                                                                 165
     Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
20
                      170
                                           175
                                                                180
     Ala Ile Ile Met Ile Met Phe $er Gly Val Asp Ala
                      185
                                           190
           INFORMATION FOR SEQ ID NO:91:
      (2)
25
           (i)
                     SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH:
                                    192 amino acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                          unknown
                      (D)
                           TOPOLOGY
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                      (A)
                           ORGANISM
                                      homosapiens
30
                      (C)
                           INDIVIDUAL ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:91:
     Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
```

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu 25 His Leu Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Thr Ser 35 40 Arg Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Ala His Pro 50 55 60 Gly Ala Pro Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val 5 Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys 80 85 Gly Gly Ala Phe Leu Met Gly Gln Met Ile Thr Phe Arg Pro Arg 95 100 105 Arg His Trp Thr Thr Gln Glu Cys Asn Cys Ser Ile Tyr Thr Gly 110 115 120 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 10 130 135 Ser Pro Thr Thr Leu Leu Leu Ala Gln Ile Met Arg Val Pro 140 145 Thr Ala Phe Leu Asp Met Val Ala Gly Gly His Trp Gly Val Leu 155 160 Ala Gly Leu Ala Tyr Phe Ser Met Gln Gly Asn Trp Ala Lys Val 170 175 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala 15 185 190

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: | 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY unknown
- (vi) ORIGINAL SOURÇE:
 - (A) ORGANISM; homosapiens
 - (C) INDIVIDUAL ISOLATE: Z1
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

35

```
Gly Gly Val Phe Leu Val Gly Gln Leu Phe Asp Phe Arg Pro Arg
                                          100
    Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
                     110
                                          115
                                                               120
    His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
                     125
                                          130
                                                               135
    Ser Pro Thr Ser Ala Leu Ile Met Ala Gln Ile Leu Arg Ile Pro
                     140
                                          145
                                                               150
5
    Ser Ile Leu Gly Asp Leu Leu Thr Gly Gly His Trp Gly Val Leu
                     155
                                          160
    Ala Gly Leu Ala Phe Phe Ser Met Gln Ser Asn Trp Ala Lys Val
                     170
                                          175
                                                               180
    Ile Leu Val Leu Phe Leu Phe Ala Gly Val Glu Gly
                     185
```

10 (2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: Z

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp 20 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Glu His Gln Ile Leu 20 His Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser 35 Arg Cys Trp Val Ala Leu Thr Pro Thr Val Ala Val Ser Tyr Ile 50 55 25 Gly Ala Pro Leu Asp Ser Leu Arg Arg His Val Asp Leu Met Val 65 70 Gly Ala Ala Thr Val Cys \$er Ala Leu Tyr Val Gly Asp Leu Cys 85 90 Gly Gly Ala Phe Leu Val Ġly Gln Met Phe Ser Phe Gln Pro Arg 100 105 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Ala Gly 110 115 30 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 135 Ser Pro Thr Thr Leu Leu Leu Ala Gln Val Met Arg Ile Pro 140 145 150 Ser Thr Leu Val Asp Leu Leu Ala Gly Gly His Trp Gly Val Leu 155 160 165

35

J

Val Gly Leu Ala Tyr Phe Ser Met Gln Ala Asn Trp Ala Lys Val
170 175 180

Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

- 145 -

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(2) INFORMATION FOR SEQ ID NO:94:
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5 (i) SEQUENCE CHARACTERISTICS:
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- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: Z7
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Val Asn Tyr His Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp Cys Pro Asn Ser Ser Ile Met Tyr Glu Ala Glu His His Ile Leu 25 20 15 His Leu Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser 40 35 Arg Cys Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu Glu Ser Ile Arg Arg His Val Asp Leu Met Val 75 Gly Ala Ala Thr Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys 80 85 90 20 Gly Gly Val Phe Leu Val Gly Gln Met Phe Ser Phe Gln Pro Arg 100 105 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Ala Gly 110 115 120 His Val Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 135 Ser Pro Thr Thr Leu Val Leu Ala Gln Val Met Arg Ile Pro 25 140 145 Ser Thr Leu Val Asp Leu Leu Thr Gly Gly His Trp Gly Ile Leu 155 160 Ile Gly Val Ala Tyr Phe Cys Met Gln Ala Asn Trp Ala Lys Val 170 Ile Leu Val Leu Phe Leu Ty‡ Ala Gly Val Asp Ala 185 190

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown

35

30

```
(D)
                           TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                           ORGANISM:
                      (A)
                                      homosapiens
                      (C)
                           INDIVIDUAL ISOLATE:
                                                 DK13
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:95:
 5
      Tyr Asn Tyr Arg Asn Ser Ser Gly Val Tyr His Val Thr Asn Asp
      Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Asp Tyr His Ile Leu
      His Leu Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Lys Ser
      Thr Cys Trp Val Ser Leu Thr Pro Thr Val Ala Ala Gln His Leu
10
      Asn Ala Pro Leu Glu Ser Leu Arg Arg His Val Asp Leu Met Val
                                            70
                       65
                                                                  75
      Gly Gly Ala Thr Leu Cys Ser Ala Leu Tyr Ile Gly Asp Val Cys
      Gly Gly Val Phe Leu Val Gly Gln Leu Phe Thr Phe Gln Pro Arg
                       95
                                           100
                                                                105
15
     Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Thr Gly
                                           115
                                                                120
     His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                      125
                                           130
      Ser Pro Thr Ala Thr Leu Val Leu Ala Gln Leu Met Arg Ile Pro
                      140
                                           145
                                                                150
      Gly Ala Met Val Asp Leu Ļeu Ala Gly Gly His Trp Gly Ile Leu
                      155
                                           160
20
      Val Gly Ile Ala Tyr Phe Ser Met Gln Ala Asn Trp Ala Lys Val
                      170
                                           175
                                                                180
      Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
                      185
      (2)
           INFORMATION FOR SEQ ID NO:96:
25
           (i)
                     SEQUENCE CHARACTERISTICS:
                          LENGTH:
                      (A)
                                   192 amino acids
                          TYPE:
                      (B)
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                          unknown
                      (D)
                          TOPOLOGY:
                                      unknown
                     ORIGINAL SOURCE:
           (vi)
                     (A)
                          ORGANISM:
                                      homosapiens
30
                     (C)
                           INDIVIDUAL ISOLATE:
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:96:
     Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
35
```

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Ser Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asp Asn Val Ser 40 Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Thr Phe Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala 65 70 5 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys 85 90 Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg 105 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly 110 115 120 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 10 125 130 Ser Pro Thr Thr Ala Leu Leu Met Ala Gln Met Leu Arg Ile Pro 140 145 150 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu 155 160 Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val 170 175 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Gly 15 185

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: SA4
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
20 25 30

His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asp Asn Val Ser
35 40 45

Lys Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu
50 55 60

Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
65 70 75

Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
80 85

35

Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg 95 100 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly 110 115 120 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 135 Ser Pro Thr Thr Ala Leu Leu Met Ala Gln Leu Leu Arg Ile Pro 140 145 5 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu 155 160 Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val 170 175 180 Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala 185 190 10 (2) INFORMATION FOR SEQ ID NO:98: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 192 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGÝ: unknown 15 (vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98: Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp 20 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu 20 25 His Ala Pro Gly Cys Val Pro Cys Val Lys Glu Gly Asn Val Ser 35 40 Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu 50 55 60 25 Gly Ala Val Thr Ala Pro Leu Arg Arg Val Val Asp Tyr Leu Ala 70 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys 85 90 Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg 100 105 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly 110 115 120 30 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 125 130 135 Ser Pro Thr Thr Ala Leu Val Met Ala Gln Val Leu Arg Ile Pro 140 145 150 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu 155 160 165

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372577_1

```
Phe Ala Val Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
                       170
                                            175
      Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Gly
                       185
      (2)
           INFORMATION FOR SEQ ID NO:99:
           (i)
                      SEQUENCE CHARACTERISTICS:
 5
                      (A)
                           LENGTH:
                                    192 amino acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                          unknown
                      (D)
                           TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                           ORGANISM:
                      (A)
                                      homosapiens
10
                      (C)
                           INDIVIDUAL ISOLATE:
                                                 SA6
           (xi)
                     SEQUENCE DE$CRIPTION: SEQ ID NO:99:
      Val Pro Tyr Arg Asn Ala Set Gly Val Tyr His Val Thr Asn Asp
      Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu
                        20
15
      His Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser
                        35
                                             40
      Arg Cys Trp Val His Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu
                        50
      Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
      Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
                                             85
                                                                  90
20
      Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
                       95
                                            100
                                                                 105
      Gln His Ala Thr Val Gln A$p Cys Asn Cys Ser Ile Tyr Ser Gly
                      110
                                            115
                                                                 120
     His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp
                      125
                                            130
                                                                 135
      Ser Pro Ala Thr Ala Leu Val Met Ala Gln Met Leu Arg Ile Pro
25
                      140
                                            145
                                                                 150
     Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
                      155
                                           160
      Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
                      170
                                            175
                                                                 180
     Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
                      185
                                            190
30
      (2)
           INFORMATION FOR SEQ ID NO:100:
           (i)
                     SEQUENCE CHARACTERISTICS:
                      (A)
                          LENGTH:
                                    192 amino acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                          unknown
35
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(D)
                           TOPOLOGY:
                                      unknown
           (vi)
                     ORIGINAL SOURCE:
                           ORGANĮSM:
                      (A)
                                      homosapiens
                           INDIVIDUAL ISOLATE:
                      (C)
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:100:
 5
     Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
      Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
     His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asn Asn Val Ser
      Arq Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu
10
      Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
                                             70
                                                                  75
                        65
      Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
                                             85
      Gly Ala Val Phe Leu Val Gly Gln Met Phe Ser Tyr Arg Pro Arg
                                            100
                        95
                                                                 105
15
      Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
                                            115
      His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
                       125
                                            130
                                                                 135
      Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
                                            145
                       140
                                                                 150
      Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
                      155
                                            160
20
      Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
                      170
                                            175
                                                                 180
      Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
                      185
      (2)
           INFORMATION FOR SEQ ID NO:101:
25
           (i)
                      SEQUENCE CHARACTERISTICS:
                           LENGTH:
                      (A)
                                    192 amino acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS:
                                          unknown
                           TOPOLOGY:
                      (D)
                                      unknown
                     ORIGINAL SOURCE:
           (vi)
30
                           ORGANISM:
                      (A)
                                      homosapiens
                      (C)
                           INDIVIDUAL ISOLATE:
                                                 SA13
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:101:
     Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
                                             10
35
```

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala 5 65 70 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys 85 Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Ser Pro Arg 105 Arg His Asn Val Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly 110 115 120 His Ile Thr Gly His Arq Met Ala Trp Asp Met Met Asn Trp 10 125 Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro 140 145 Gln Val Val Ile Asp Ile Iḷe Ala Gly Ala His Trp Gly Val Leu 155 160 Phe Ala Ala Ala Tyr Tyr Ala Ser Ala Ala Asn Trp Ala Lys Val 170 175 180 15 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala 185

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Leu Thr Tyr Gln Asn Ser Ser Gln Leu Tyr His Leu Thr Asn Asp

1 10 15

Cys Pro Asn Ser Ser Ile Val Leu Glu Ala Asp Ala Met Ile Leu
20 25 30

His Leu Pro Gln Cys Leu Pro Cys Val Arg Val Asp Asp Arg Ser
35 40 45

Thr Cys Trp His Ala Val Thr Pro Thr Leu Ala Ile Pro Asn Ala
50 55 60

Ser Thr Pro Ala Thr Gln Phe Arg Arg His Val Asp Leu Leu Ala
65 70 75

Gln Ala Ala Val Val Cys Ser Ser Leu Tyr Ile Gln Asp Leu Cys
80 85

35

30

20

						- 0								
	Gln Se	r Leu	Phe	Leu 95	Ala	Gln	Gln	Leu	Phe 100	Thr	Phe	Gln	Pro	Arg 105
	Arg Hi	s Trp	Thr		Gln	Asp	Cys	Asn		Ser	Ile	Tyr	Thr	
	His Va	l Thr	Gln		Arg	Met	Ala	Trp	-	Met	Met	Met	Asn	
5	Ser Pr	o Thr	Thr		Leu	Val	Leu	Ser		Ile	Leu	Arg	Val	
	Glu Il	e Cys	Ala	Ser 155	Val	Ile	Phe	Gln		His	Trp	Gln	Ile	
	Leu Al	a Val	Ala		Phe	Gln	Met	Ala		Asn	Trp	Leu	Lys	
	Leu Al	a Val	Leu		Leu	Phe	Ala	Gln		Glu	Ala			
10				>										
	(2)	INFOR	MATI	ON FO	OR SI	EQ II	ои с	: 103	3:					
		(i)		(A)	LEI	NGTH	: 5		ase p	pairs	5			
				(B)	TYI			leic						
15				(C) (D)		O LO	EDNES GY:	line	sing ear	уте				
		(vi)		ORIO	TNAI	Sot	TRCE							
		,,		(A) (C)	ORG	GANIS	SM:	homo ISOI			۲7			
		(xi)		(A) (C)	ORO	GANIS DIVII	SM: DUAL	homo	LATE): 10	03:	
20	ATG AG	(xi)		(A) (C) SEQU	ORC INI JENCI	GANIS DIVII E DES	SM: DUAL SCRII	homo ISOI TIOI	TATE	: DF SEQ 1	ID NO		03:	39
20	ATG AG	(xi) C ACG C AAC	AAT CGT	(A) (C) SEQU	ORC INI JENCI AAA CCA	GANIS DIVII DES CCT CAG	SM: DUAL SCRII CAA GAC	homo ISOI PTION AGA GTC	LATE: N: S AAA AAG	E DE EEQ I ACC TTC	D NO AAA CCG	CGT GGT	03:	39 78
20	AAC AC GGC GG	(xi) C ACG C AAC T CAG	AAT CGT ATC	(A) (C) SEQU CCT CGC GTT	ORC INI JENCI AAA CCA GGT	E DES CCT CAG GGA	SM: DUAL SCRII CAA GAC GTT	homo ISOI PTION AGA GTC TAC	LATE: AAA AAG TTG	E DE SEQ I ACC TTC TTG	ID NO AAA CCG CCG	CGT GGT CGC	03:	78 117
20	AAC AC GGC GG AGG GG	(xi) C ACG C AAC T CAG C CCT	AAT CGT ATC AGA	(A) (C) SEQU CCT CGC GTT TTG	ORC INI JENCI AAA CCA GGT GGT	E DES CCT CAG GGA GTG	SM: DUAL SCRII CAA GAC GTT CGC	homo ISOI PTION AGA GTC TAC GCG	AAA AAG TTG CCG	E DE SEQ D ACC TTC TTG AGG	AAA CCG CCG AAG	CGT GGT CGC ACT	03:	78 117 156
20	AAC AC GGC GG AGG GG TCC GA CCC AA	(xi) C ACG C AAC T CAG C CCT G CGG G GCA	AAT CGT ATC AGA TCG CGT	(A) (C) SEQU CCT CGC GTT TTG CAA CGG	ORCINI JENCI AAA CCA GGT GGT CCT CCC	CCT CAG GGA GTG CGA GAG	SM: DUAL CAA GAC GTT CGC GGT GGC	homo ISOI PTION AGA GTC TAC GCG AGA AGG	AAA AAG TTG CCG CGT ACC	E DE SEQ D ACC TTC TTG AGG CAG TGG	AAA CCG CCG AAG CCT GCT	CGT GGT CGC ACT ATC CAG	03:	78 117
	AAC AC GGC GG AGG GG TCC GA CCC AA CCC GG	(xi) C ACG C AAC T CAG C CCT G CGG G GCA G TAC	AAT CGT ATC AGA TCG CGT CCT	(A) (C) SEQU CCT CGC GTT TTG CAA CGG TGG	ORCINI JENCE AAA CCA GGT GGT CCT CCC CCC	CCT CAG GGA GTG CGA GAG CTC	EM: DUAL CAA GAC GTT CGC GGT GGC TAT	HOMO ISOI PTION AGA GTC TAC GCG AGA AGG GGC	AAA AAG TTG CCG CGT ACC AAT	E DESEQ DESERTED TO THE AGG CAG TGG GAG	AAA CCG CCG AAG CCT GCT GGC	CGT GGT CGC ACT ATC CAG TGC	03:	78 117 156 195 234 273
20	AAC AC GGC GG AGG GG TCC GA CCC AA CCC GG GGG TG	(xi) C ACG C AAC T CAG C CCT G CGG G GCA G TAC G GCG	AAT CGT ATC AGA TCG CGT CCT GGA	(A) (C) SEQU CCT CGC GTT TTG CAA CGG TGG	ORCINI JENCI AAA CCA GGT GGT CCT CCC CTC	CCT CAG GGA GTG CGA GAG CTC CTG	SM: DUAL CAA GAC GTT CGC GGT GGC TAT TCT	HOMO ISOI PTION AGA GTC TAC GCG AGA AGG GGC CCC	AAA AAG TTG CCG CGT ACC AAT CGT	E DI SEQ I ACC TTC TTG AGG CAG TGG GAG GAG GGC	AAA CCG CCG AAG CCT GCT GCC TCT	CGT GGT CGC ACT ATC CAG TGC CGG	03:	78 117 156 195 234 273 312
	AAC AC GGC GG AGG GG TCC GA CCC AA CCC GG GGG TG CCT AG AAT TT	(xi) C ACG C AAC T CAG C CCT G CGG G TAC G TGG G TGG G TGG	AAT CGT ATC AGA TCG CGT CCT GGA GGC AAA	(A) (C) SEQU CCT CGC GTT TTG CAA CGG TGG TGG CCC GTC	ORCINI JENCI AAA CCA GGT GGT CCC CCC CCC ACA ATC	CCT CAG GGA GTG CGA GAG CTC CTG GAC GAT	EM: DUAL CAA GAC GTT CGC GGT GGC TAT TCT CCC ACC	HOMO ISOI PTION AGA GTC GCG AGA AGG GGC CCC CGG CTT	AAA AAG TTG CCG CGT ACC AAT CGT CGC ACG	ACC TTC TTG AGG CAG TGG GAG GGC AGG	AAA CCG CCG AAG CCT GCT GGC TCT TCG GGC	CGT GGT CGC ACT ATC CAG TGC CGG CGC	03:	78 117 156 195 234 273 312 351 390
	AAC ACGGC GGGGGGGGAATTTTGCC GA	(xi) C ACG C AAC T CAG C CCT G CGG G GCA G TAC G GCG G TGG C TGG C TCC	AAT CGT ATC AGA TCG CGT CCT GGA GGC AAA ATG	(A) (C) SEQUE CCT CGC GTT TTG CAA CGG TGG CCC GTC GGG	ORCINI JENCE AAA CCA GGT CCT CCC CTC ACA ATC TAC	CCT CAG GGA GTG CGA GAG CTC CTG GAC GAT ATA	EM: DUAL CAA GAC GTT CGC GGT TCT CCC ACC CCG	HOMO ISOI PTION AGA GTC TAC GCG AGA AGG CCC CCG CTT CTC	AAA AAG TTG CCG CGT ACC AAT CGT CGC ACG GTC	ACC TTC TTG AGG CAG TGG GAG GGC AGG TGC	AAA CCG CCG AAG CCT GCT GGC TCT TCG GGC	CGT GGT CGC ACT ATC CAG TGC CGG CGC TTC	03:	78 117 156 195 234 273 312 351 390 429
	AAC AC GGC GG AGG GG TCC GA CCC AA CCC GG GGG TG CCT AG AAT TT	(xi) C ACG C AAC T CAG G CGG G GCA G TAC G GGG C TGG G GGT C CTC A GGC	AAT CGT ATC AGA TCG CGT CCT GGA GGC AAA ATG GCT	(A) (C) SEQUE CCT CGC GTT TTG CAA CGG TGG CCC GTC GGG GCC	ORCINI JENCI AAA CCA GGT CCT CCC CTC ACA ATC TAC AGG	CCT CAG GGA GTG CTC GAC CTG GAC CTG GAC GAT ATA	EM: DUAL CAA GAC GTT CGC GGT TCT CCC ACC CCG CTG	HOMO ISOI PTION AGA GTC TAC GCG AGA AGG CCC CGG CTT CTC GCG	AAA AAG TTG CCG CGT ACC AAT CGT CGC ACG GTC CAT	ACC TTC TTG AGG CAG TGG GAG GGC AGG TGC GGC	AAA CCG CCG AAG CCT GCT GGC TCT TCG GGC GCC	CGT GGT CGC ACT ATC CAG TGC CGG CGC TTC CCT	03:	78 117 156 195 234 273 312 351 390
	AAC AC GGC GG AGG GG TCC GA CCC AA CCC GG GGG TG CCT AG AAT TT GCC GA CTT GG GTT CT CCT GG	(xi) C ACG C AAC T CAG G CCT G GCG G TAC G TGG G GCT C CTC A GGC TGC	AAT CGT ATC AGA TCG CGT CCT GGA ATG GCT GAC TCT	(A) (C) SEQUE CCT CGC GTT TTG CAA CGG TGG CCC GTC GGG GCC GTC GGG GCC TTC	JENCE AAA CCA GGT CCC CCC ACA ATC AGG GTG TCT	E DES CCT CAG GGA GTG CTC GAC CTC GAC GAC ATA ATA	EM: DUAL CAA GAC GTT CGC GGT TCT CCC ACC CCG CTG TAT TTC	AGA GTC TAC GCG AGA AGG GCC CCC CGG CTT CTC GCG GCA CTT	AAA AAG TTG CCG CGT ACC AAT CGC ACG GTC CAT ACA	ACC TTC TTG AGG CAG TGG GAG GGC AGG TGC GGC GGC	AAA CCG CCG AAG CCT GCT TCT TCG GGC GCC GCC	CGT GGT CGC ACT ATC CAG TGC CGG CGC TTC CCT CGG	03:	78 117 156 195 234 273 312 351 390 429 468 507 546
	AAC AC GGC GG AGG GG CCC AA CCC GG GGG TG CCT AG AAT TT GCC GA CTT GG GTT CT	(xi) C ACG C AAC T CAG G CCT G GCG G TAC G TGG G GCT C CTC A GGC TGC	AAT CGT ATC AGA TCG CGT CCT GGA ATG GCT GAC TCT	(A) (C) SEQUE CCT CGC GTT TTG CAA CGG TGG CCC GTC GGG GCC GTC GGG GCC TTC	JENCE AAA CCA GGT CCC CCC ACA ATC AGG GTG TCT	E DES CCT CAG GGA GTG CTC GAC CTC GAC GAC ATA ATA	EM: DUAL CAA GAC GTT CGC GGT TCT CCC ACC CCG CTG TAT TTC	AGA GTC TAC GCG AGA AGG GCC CCC CGG CTT CTC GCG GCA CTT	AAA AAG TTG CCG CGT ACC AAT CGC ACG GTC CAT ACA	ACC TTC TTG AGG CAG TGG GAG GGC AGG TGC GGC GGC	AAA CCG CCG AAG CCT GCT TCT TCG GGC GCC GCC	CGT GGT CGC ACT ATC CAG TGC CGG CGC TTC CCT CGG	03:	78 117 156 195 234 273 312 351 390 429 468 507

SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid

35

(i)

		·	
٥	(C (D) STRANDEDNESS: single) TOPOLOGY: linear	
	(vi) OR (A (C		
5	(xi) SE	QUENCE DESCRIPTION: SEQ ID NO: 104:	
10	AAC ACC AAC CGT CGGGC GGT CAG ATC GTAG GGC CCT AGA TTAG GCC AAG GCA CGT CGCC AAG TAC CCT TGGGG TGG GGA TGCCT AGC TGG GGC CCC AAT TTG GGT AAG GT	T AAA CCT CAA AGA AAA ACC AAA CGT C CCA CAG GAC GTC AAG TTC CCG GGT T GGT GGA GTT TAC TTG TTG CCG CGC G GGT GTG CGC GCG ACG AGG AAG ACT A CCT CGA GGT AGA CGT CAG CCT ATC G CCC GAG GGC AGG ACC TGG GCT CAG G CCC CTC TAT GGC AAT GAG GGC TGC G CTC CTG TCT CCC CGT GGC TCT CGG C ACG GAC CCC CGG CGT AGG TCG CGC C ATC GAT ACC CTT ACG TGC GGC TTC G TAC ATA CCG CTC GTC GGC GCC CCT	39 78 117 156 195 234 273 312 351 390 429
15	CTC GGA GGC GCT GC GTT CTG GAA GAC GG	C AGG GCC CTG GCG CAT GGC GTC CGG C GTG AAC TAT GCA ACA GGG AAC CTT C TCT ATC TTC CTT CTG GCC CTG CTC	468 507 546 573
	(2) INFORMATION	FOR SEQ ID NO: 105:	
20	(i) SE (A (B (C (D) TYPE: nucleic acid) STRANDEDNESS: single	
25	(A (C		
30	AAC ACC AAC CGT CG GGC GGT CAG ATC GT AGG GGC CCT AGA TT TCC GAG CGG TCG CA CCC AAG GCA CGT CG CCC GGG TAT CCT TG GGG TGG GCG GGA TG CCT AGC TGG GGC CC AAT TTG GGT AAG GT GCC GAC CTC ATG GG	T AAA CCT CAA AGA AAA ACC AAA CGT C CCA CAG GAC GTC AAG TTC CCG GGT T GGT GGA GTT TAC TTG TTG CCG CGC G GGT GTG CGC GCG ACG AGG AAG ACT A CCT CGA GGT AGA CGT CAG C CCC GAG GGC AGG ACC TGG GCT CAG C CCC CTC TAT GGC AAT GAG GGC TGC C CTC CTG TCT CCC CGT GGC TCT CGG C ACA GAC CCC CGG CGT AGG TCG CGC C ATC GAT ACC CTC ACG TGC GGC TTC G TAC ATA CCG CTC GTC GGC GCC CCC C AGG GCC CTG GCC CAT GGC GCC CCC C AGG GCC CTG GCC CCC C AGG GCC CTG GCC CCC	39 78 117 156 195 234 273 312 351 390 429 468
35	372577_1		

0			
	GTT CTG GAA GAC GGC GTG AAC TAT GCA ACA GG CCT GGT TGC TCT TTC TCT ATC TTC CTC CTA GC TCT TGC CTG ACT GTG CCC GCT TCA GCC		507 546 573
	(2) INFORMATION FOR SEQ ID NO: 106:		
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pai (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
10	(vi) ORIGINAL SOURCE: (A) ORGANI\$M: homosapien (C) INDIVIDUAL ISOLATE:	ns SW1	
*	(xi) SEQUENCE DESCRIPTION: SEQ) ID NO: 106:	
15	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA AC AAC ACC AAC CGT CGC CCA CAG GAC GTC AAG TT GGC GGT CAG ATC GTT GGT GGA GTT TAC TTG TT AGG GGC CCT AGA TTG GGT GTG CGC GCG ACG ACG TCC GAG GGC AGG ACC TCC AAG GCG CGT CGG CCC GAG GGC AGG ACC TCCC GAG GCG TAT CCT TGG CCC CTC TAT GGC AAT GAG GGA TGG GCC CTC TCC CCC CGT GCC CCT AGC TCC CCC CGT GCC CCT AGC TGC CCC CGT AGC CCT AGC TGC CCC CGT ACC	CC CCG GGT CG CCG CGC GG AAG ACT AG CCT ATC GG GCT CAG AG GGC TGC GC TCT CGG	39 78 117 156 195 234 273 312 351
20	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACG TG GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GC CTT GGA GGC GCT GCC AGG GCC CTG GCG CAT GC GTT CTG GAA GAC GGC GTG AAC TAT GCA ACA GC CCT GGT TGC TCT TTC TCT ATC TTC CTT CTG GC TCT TGC CTG ACA GTG CCC GCG TCA GCC	GC GGC TTC GC GCC CCT GC GTC CGG GG AAC CTT	390 429 468 507 546 573
25	(2) INFORMATION FOR SEQ ID NO: 107:		
23	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pai (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapien (C) INDIVIDUAL ISOLATE:	ıs S18	
	(xi) SEQUENCE DESCRIPTION: SEQ) ID NO: 107:	
35	ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA AC AAC ACC AAC CGT CGC CCA CAG GAC GTT AAG TT	CC AAA CGT CC CCG GGT	39 78

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GGC GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC
                                                                  117
      AGG GGC CCT AGA TTG GGT GTG CGC GCG ACG AGG AAG ACT
                                                                 156
      TCC GAG CGG TCG CAA CCT CGC GGT AGA CGT CAG CCT ATC
      CCC AAG GCG CGT CGG CCC GAG GGC AGG ACC TGG GCT CAG
                                                                 234
      CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TGC
                                                                 273
      GGG TGG GCG GGA TGG CTC CTG TCC CCC CGT GGC TCC CGG
                                                                 312
      CCT AGC TGG GGC CCT ACA GAC CCC CGG CGT AGG TCG CGC
                                                                 351
 5
      AAT TTG GGC AAA GTC ATC GAT ACC CTC ACG TGC GGC TTC
                                                                 390
      GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCT
                                                                 429
      CTC GGA GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG
      GTT CTG GAA GAC GGC GTG AAC TAT GCA ACA GGG AAC CTT
                                                                 507
      CCT GGT TGC TCT TTC TCT ATC TTC CTT CTG GCC CTG CTC
                                                                 546
      TCT TGT CTG ACT GTG CCC GCG TCA GCT
                                                                  573
10
      (2)
            INFORMATION FOR SEQ ID NO: 108:
             (i)
                      SEQUENCE CHARACTERISTICS:
                       (A)
                            LENGTH: 573 base pairs
                       (B)
                            TYPE: nucleic acid
                       (C)
                            STRANDEDNESS: single
                       (D)
                            TOPOLOGY:
                                       linear
15
             (vi)
                      ORIGINAL SOURCE:
                       (A)
                            ORGANISM:
                                       homosapiens
                       (C)
                            INDIVIDUAL ISOLATE:
             (xi)
                      SEQUENCE DESCRIPTION: SEQ ID NO: 108:
     ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT
                                                                   39
20
     AAC ACC AAC CGT CGC CCA GAG GAC GTC AAG TTC CCG GGT
                                                                  78
     GGC GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC
                                                                 117
     AGG GGC CCT AGA TTG GGT GTG CGC GCG ACG AGG AAG ACT
                                                                 156
     TCC GAG CGG TCG CAA CCT CGA GGT AGA CGT CAG CCT ATC
                                                                 195
      CCC AAG GCG CGT CGG CCC GAG GGC AGG ACC TGG GCT CAG
                                                                 234
     CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TGC GGG TGG GCG GGA TGG CTC CTG TCC CCC CGT GGC TCT CGG
                                                                 273
                                                                 312
25
      CCT AGC TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGC
                                                                 351
     AAT TTG GGT AAG GTC ATC GAC ACC CTC ACG TGC GGC TTC
     GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC
                                                                 429
      CTT GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGA
                                                                 468
     GTT CTG GAA GAC GGC GTG AAC TAT GCA ACA GGG AAT CTT
                                                                 507
                              ATC TTC CTT TTG GCT TTG CTC
      CCT GGT TGC TCT TTC TCT
                                                                 546
     TCT TGC TTG ACC GTG CCC GCA TCG GCC
                                                                  573
30
            INFORMATION FOR $EQ ID NO: 109:
      (2)
                      SEQUENCE CHARACTERISTICS:
             (i)
                           LENGTH: 573 base pairs
                       (A)
                       (B)
                            TYPE: nucleic acid
                       (C)
                            STRANDEDNESS: single
35
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		- 156 -	
0		(D) TOPOLOGY linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA10	
5	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 109:	
10	AAC ACC AAC CGC GGT GGT CAG ATC AGG GGC CCC AGG TCC GAG CGG TCG CCC AAG GCT CGC CCC GGG TAC CCT GGG TGG GCA GGA CCT AGT TGG GGC AAT TTG GGT AAG GCC GAC CTC ATG TTA GGG GGC GCT GTT CTG GAA GAC CCC GGT TGC CCT	CCT AAA CCT CAA AGA AAA ACC AAA CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GTT GGT GGA GTC TAT CTG TTG CCG CGC TTG GGT GTG CGC GCG ACG AGG AAG ACT CAA CCT CGT GGA AGG CGA CAA CCT ATC CAG CCC GAG GGC AGG ACC TGG GCC CAG TGG CCC CTC TAT GGC AAT GAG GGC TTG TGG CTC CTG TCA CCC CGT GGC TCT CGG CCC ACG GAC CGC CGG CGT AGG TCG CGT GTC ATC GAT ACC CTC ACA TGC GGC TTC GGG TAC ATT CCG CTC GTC GGC GCC CCT GCC AGG GCC TTG GCG CAT GGC GCC CCT GCC AGG GCC TTG GCG CAT GGC GCC CCT GCC AGG GCC TTG GCG CAT GGC GTC CGG GGC GTG AAC TAT GCA ACA GGG AAT TTG TTC TCT ATC TTC CTC TTG GCT TTG CTG ATC CCA GCT TCC GCT	39 78 117 156 195 234 273 312 350 429 468 507 546 573
20		SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANIȘM: homosapiens (C) INDIVIDUAL ISOLATE: S45	
25	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 110:	
30	AAC ACC AAC CGC GGC GGT CAG ATC AGG GGC CCC AGG TCC GAG CGG TCA CCC AAG GCT CGC CCC GGG CAT CCT GGG TGG GCA GGA CCT AGT TGG GGC AAT TTG GGT AAG GCC GAC CTC ATG CTA GGG GGC GCT	CCT AAA CCT CAA AGA CAA ACC AAA CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT GTT GGT GGA GTT TAC CTG TTG CCG CGC TTG GGT GTG CGC GCG ACT AGG AAG ACT CAA CCT CGT GGA CGG CGA CAA CCT ATC CGG CCC GAG GGC AGG GCC TGG GCC CAG TGG CCC CTC TAT GGC AAT GAG GGC TTG TGG CTC CTG TCA CCC CGT GGC TCC CGG CCC ACG GAC CCC CGG CGT AGG TCG CGC GTC ATC GAT ACC CTC ACG TGC GGC TTC GGG TAC ATT CCG CTC GTC GGC GCC GCC AGA GCC TTG GCC CCC GCC AGA GCC TTG GCC CCC	39 78 117 156 195 234 273 312 351 390 429 468
35		GGC GTG AAC TAT GCA ACA GGG AAT CTG	507

0	- 157 -	
	CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT CTG TCC TGC TTG ACC ATC CCA GCT TCC GCT	546 573
	(2) INFORMATION FOR SEQ ID NO: 111:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: D1	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:	
15 20	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC AGG GGC GGC GGC GGC GGC GGC GG	39 78 117 156 195 234 273 312 351 390 429 468 507 546 573
	(2) INFORMATION FOR SEQ ID NO: 112:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: US6	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:	
35	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	39 78 117 156

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5	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC CCC AAG GCT CGC CGG CCC GAG GGC AGG GCC TGG GCT CAG CCC GGG TAC CCT TGG CCC CTC TAT GGC AAC GAG GGC ATG GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCC CGG CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC GCC GAC CTC ATG GGC GCC CCC CTA GGG GCC CCC CTA GGG GCC CCC CTA GGG GCC GCC CCC CTA GGG GGC GCT GCC AGG GCC TTG GCG CAT GGC GCC CCC CTA GGG GGC GCC AGG GCC TTG GCG GAC CTC ACA TGC GCC CCC CTA GGG GGC GTC ACA TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG CTG TCC TGT TTG CTG TCC TGT TTG ACC ATT CCA GCT TCC GCT	195 234 273 312 351 390 429 468 507 546 573
	(2) INFORMATION FOR SEQ ID NO: 113:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY linear	
15	(vi) ORIGINAL SOURCE:	
13	(A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: P10	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:	
20	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC CCC AAG GCT CGC CGC GAG GCC AGG GCC TGG GCT CAG	39 78 117 156 195 234
	CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TTG GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCT CGG	273 312
	CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	351 390
25	GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG	429 468
	GTT CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT CTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG CTG	507
	TCC TGC CTG ACC ATC CCA GCG TCC GCT	546 573
30	(2) INFORMATION FOR SEQ ID NO: 114:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
25	(D) TOPOLOGY: linear	
35		

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	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: DK1
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 114:
5	AAC ACC AAC CGC GGT GGT CAG ATC AGG GGC CCC AGG TCC GAG CGG TCG	CCT AAA CCT CAA AGA AAA ACC AAA CGT 39 CGC CCA CAG GAC GTC AAG TTC CCG GGC 78 GTT GGT GGA GTT TAC CTG TTG CCG CGC 117 TTG GGT GTG CGC GCG ACT AGG AAG ACT 156 CAA CCT CGT GGA AGG CGA CAA CCT ATC 195 CGG CCC GAG GGC AGG GCC TGG GCT CAG 234
10	CCC GGG TAC CCT GGG TGG GCA GGA CCT AGT TGG GGC AAT TTG GGT AAG GCC GAC CTC ATG CTA GGG GGC GCT GTT CTG GAG GAC CCC GGT TGC TCT	TGG CCC CTC TAT GGC AAT GAG GGC ATG 273 TGG CTC CTG TCA CCC CGC GGC TCT CGG 312 CCC AAC GAC CCC CGG CGT AGG TCG CGT 351 GTC ATC GAT ACC CTC ACA TGC GGC TTC 390 GGG TAC ATT CCG CTC GTC GGC GCC CCC 429 GCC AGG GCC CTG GCG CAT GGC GTC CGG 468 GGC GTG AAC TAC GCA ACA GGG AAT TTG 507 TTC TCT ATC TTC CTC TTG GCT CTG TTG 546 ATC CCA GCT TCC GCC 573
15	(2) INFORMATION	ON FOR SEQ ID NO: 115:
20	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
20	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: T10
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 115:
25	AAC ACC AAC CGC GGT GGT CAG ATC AGG GGC CCC AGG TCC GAG CGG TCG CCC AAG GCT CGC CCC GGG TAC CCT	CCT AAA CCT CAA AGA AAA ACC AAA CGT 39 CGC CCA CAG GAC GTC AAG TTC CCG GGC 78 GTT GGT GGA GTT TAC CTG TTG CCG CGC 117 TTG GGT GTG CGC GCG ACT AGG AAG ACT 156 CAA CCT CGT GGA AGG CGA CAG CCT ATC 195 CAG CCC GAG GGC AGG GCC TGG GCT CAG 234 TGG CCC CTC TAT GGC AAT GAG GGC ATG 273
30	CCT AGT TGG GGC AAT TTG GGT AAG GCC GAC CTC ATG CTA GGG GGC GCT GTT CTG GAG GAC CCC GGT TGC TCT	TGG CTC CTG TCA CCC CGT GGC TCC CGG 312 CCC ACA GAC CCC CGG CGT AGG TCG CGT 351 GTC ATC GAT ACC CTC ACA TGC GGC TTC 390 GGG TAC ATT CCG CTC GTC GGC GCC CCC 429 GCC AGG GCT CTG GCA CAT GGT GTC CGG 468 GGC GTG AAC TAT GCA ACA GGG AAT TTG 507 TTT TCT ATC TTC CTC TTG GCT CTG CTG 546 ATC CCA GCT TCC GCT 573
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	(2) INFORMATION	ON FOR SEQ ID NO: 116:	
5	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SW2	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 116:	
10	AAC ACC AAC CGC	CCT AAA CCT CAA AGA AAA ACC AAA CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GTT GGT GGA GTT TAC CTG TTG CCG CGC	39 78 117
15	AGG GGC CCC CGG TCC GAG CGG TCG CCC AAG GCT CGC CCT GGG TAC CCC GGA TGG GCA GGA CCT AGT TGG GGC AAT TTG GGT AAG GCC GAC CTC ATG CTA GGG GGC GCT GTC CTG GAG GAC	TTG GGT GTG CGC GCG ACT AGG AAG ACT CAA CCT CGT GGA AGG CGA CAA CCT ATC CAG CCC GAG GGC AGG GCC TGG GCT CAG TGG CCC CTC TAT GGC AAT GAG GGC ATG TGG CTC CTG TCC CCC CGC GGC TCT CGG CCC ACT GAC CCC CGG CGT AGG TCG CGT GTC ATC GAT ACC CTC ACA TGC GGC TTC GGG TAC ATT CCG CTC GTC GGC GCC CCC GCC AGG GCC CTG GCG CAT GGC GTC CGG GCC AGG GCC CTG GCG CAT GGC GTC CGG GGC GTG AAC TAT GCA ACA GGG AAT CTG	156 195 234 273 312 351 390 429 468 507
20		TTT TCT ATC TTC CTC TTG GCT TTG CTG ATC CCA GCT TCC GCT	546 573
20			
٠	(2) INFORMATION	ON FOR SEQ ID NO: 117:	
25	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: IND3	
30	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 117:	
	AAC ACC AAC CGC GGT GGC CAG ATC AGG GGC CCC AGG TCC GAG CGG TCG	CCT AAA CCT CAA AGA AAA ACC AAA CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GTT GGT GGA GTT TAC CTG TTG CCG CGC TTG GGT GTG CGC GCG ACT AGG AAG ACT CAA CCT CGT GGA AGG CGA CAA CCT ATC CGG CCC GAG GGT AGG GCC TGG GCT CAG	39 78 117 156 195 234
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5	GGG TGG GCA GGA CCT AGT TGG GGC AAT TTG GGT AAA GCC GAC CTC ATG CTA GGG GGC GCT GTC CTG GAG GAC CCC GGT TGC TCT TCC TGT TTG ACC	TGG CCC CTC TAT GGC AAT GAG GGC TTG TGG CTC CTG TCA CCC CGC GGT TCT CGG CCC ACA GAC CCC CGG CGT AGG TCG CGT GTC ATC GAT ACC CTC ACA TGC GGC TTC GGG TAC ATC CCG CTC GTC GGC GCC CCC GCC AGG GCC CTG GCG CAT GGC GTC CGG GGC GTG AAC TAT GCA ACA GGG AAC TTG TTC TCT ATC TTC CTT TTA GCT TTG CTA ATC CCA GCT TCC GCT	273 312 351 390 429 468 507 546 573
10	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: \$73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: IND8	
15	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 118:	
20	AAC ACC AAC CGC GGT GGC CAG ATC AGG GGC CCC AGG TCC GAG CGG TCG CCC AAG GCT CGC CCC GGG CAC CCT GGG TGG GCA GGA CCT AGT TGG GGC AAT TTG GGT AAG GCC GAC CTC ATG CTA GGG GGT GCT GTC CTG GAG GAC	TGG CTC CTG TCA CCC CGC GGC TCT CGG CCC ACA GAC CCC CGG CGT AGG TCG CGT GTC ATC GAT ACC CTC ACA TGC GGC TTC GGG TAC ATC CCG CTC GTC GGC GCC CCC GCC AGG GCC CTG GCG CAT GGC GTC CGG GGC GTG AAC TAT GCA ACA GGG AAC TTG	39 78 117 156 195 234 273 312 351 390 429 468 507
25	CCC GGT TGC TCT TCC TGT TTG ACC	TTC TCT ATC TTC CTT TTG GCT TTG CTA GTC CCA GCT TCC GCT	546 573
	(2) INFORMATION	ON FOR SEQ ID NO: 119:	3/ 3
30	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
35	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: S9	

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	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 119:	
5	AAC ACC AAC CGC GGT GGT CAG ATC AGG GGC CCC AGG TCC GAG CGG TCG CCC AAG GCT CGC CCC GGG TAC CCT GGG TGG GCA GGA CCT AGT TGG GGC	CCT AAA CCT CAA AGA AAA ACC AAA CGT CGC CCA CAG GAC GTT AAG TTC CCG GGC GTC GGT GGA GTT TAC CTG TTG CCG CGC TTG GGT GTG CGC GCA ACT AGG AAG ACT CAA CCT CGT GGA AGG CGA CAA CCT ATC CAT CCC GAG GGC AGG GCC TGG GCT CAG TGG CCC CTC TAC GGC AAT GAG GGC TTG TGG CTC CTG TCA CCC CGT GGC TCT CGG CCC AAT GAG CCC CGG CGT AGG TCG CGT	39 78 117 156 195 234 273 312 351
10	GCC GAC CTC ATG CTA GGG GGC GCT GTT CTG GAG GAC CCC GGT TGC TCT	GTC ATC GAT ACC CTC ACA TGC GGC TTT GGG TAC ATT CCG CTC GTC GGC GCC CCC GCC AGG GCT CTG GCG CAT GGC GTC CGG GGC GTG AAC TAT GCA ACA GGG AAC CTC TTC TCT ATC TTC CTT CTG GCT TTG CTG ATC CCA GCT TCC GCT	390 429 468 507 546 573
	(2) INFORMATIO	N FOR SEQ ID NO: 120:	
15	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
20		ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: HK3	
		SEQUENCE DESCRIPTION: SEQ ID NO: 120:	
25	AAC ACC AAC CGC GGT GGT CAG ATC AGG GGC CCC AGG TCA GAG CGG TCG CCC AAG GCT CGC CCC GGG TAT CCT	CCT AAA CCT CAA AGA AAA ACC AAA CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GTT GGT GGA GTT TAC CTG TTG CCG CGC TTG GGT GTG CGC GCG ACC AGG AAG ACT CAA CCT CGT GGA AGG CGA CAA CCT ATC CAA CCC GAG GGC AGG ACC TGG GCT CAG TGG CCC CTC TAT GGC AAC GAG GGC ATG TGG CTC CTG TCA CCC CGC GGC TCT CGG	39 78 117 156 195 234 273 312
30	CCT AAT TGG GGC AAT TTG GGT AAG GCC GAC CTC ATG CTA GGG GGC GTT GTT CTG GAG GAC CCC GGT TGC TCT	CCC ACG GAC CCC CGG CGT AGG TCG CGC GTC ATC GAT ACC CTC ACG TGC GGC TTC GGG TAC AFC CCG CTC GTC GGT GCC CCC GCC AGA GCC TTG GCA CAT GGT GTC CGG GGC GTG AAC TAT GCA ACA GGG AAT TTA TTC TCT ATC TTC CTC TTG GCT TTG CTG ACC CCA GCT TCC GCT	351 390 429 468 507 546 573
	(2) INFORMATIO	N FOR SEQ ID NO: 121:	

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	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: HK5	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 121:	
10	AAC ACC AAC CGC GGT GGT CAG ATC AGG GGC CCC AGG TCC GAG CGG TCG	CCT AAA CCT CAA AGA AAA ACC AAA CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GTT GGT GGA GTT TAC CTG TTG CCG CGC TTG GGT GTG CGC GCG ACC AGG AAG ACT CAA CCT CGT GGA AGG CGA CAA CCT ATC CGA CCC GAG GGC AGG ACC TGG GCT CAG	39 78 117 156 195 234
15	AAT TTG GGT AAG GCC GAC CTC ATG CTA GGG GGC GTT GTT CTG GAG GAC CCC GGT TGC TCT	TGG CTC CTG TCA CCC CAT GGC TCT CGG CCC ACG GAC CCC CGG CGT AGG TCG CGT GTC ATC GAT ACC CTC ACG TGC GGC TTC	273 312 351 390 429 468 507 546 573
20	(2) INFORMATION	ON FOR SEQ ID NO: 122:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: HK4	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 122:	
30	AAC ACC AAC CGC GGT GGC CAG ATC AGG GGC CCC AGG CCC CCC CCC CCC CCC GGG TAC CCT	CCT AAA CCT CAA AGA AAG ACC AAA CGT CGC CCA CAG GAC GTT AAG TTC CCG GGC GTC GGT GGA GTT TAC CTG TTG CCG CGC TTG GGT GTG CGC GCG ACT AGG AAG ACT CAA CCT CGT GGA AGG CGA CAA CCT ATC CAA CCC GAG GGC AGG ACC TGG GCT CAG TGG CCC CTC TAT GGC AAT GAG GGC ATG TGG CTC CTG TCA CCC CGC GGC TCT CGG	39 78 117 156 195 234 273 312
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	CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGC	253
	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	351 390
	GCC GAC CTC ATG GGG TAC ATT/ CCG CTC GTC GGC GCC CCC	429
	TTA GGG GGC GTT GCC AGA GCC CTG GCA CAT GGT GTC CGG	468
	GTT GTG GAG GAC GGC GTG AA¢ TAT GCA ACA GGG AAT TTG	507
	CCC GGT TGC TCT TTC TCT AT¢ TTC CTC TTG GCT CTG CTG	546
5	TCC TGT TTG ACC ATC CCA GCT TCC GCT	573
	(2) INFORMATION FOR SEQ ID NO: 123:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: P8	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:	
15	ATG AGC ACG ACT CCT AAA QCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AGC CGC CCA QAG GAC GTT AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGA TCG CAA CCT ¢GT GGC AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CGG CCC GAG GGT AGG GCC TGG GCT CAG	234
	CCC GGG CAC CCT TGG CCC ¢TC TAT GCC AAT GAG GGC TTG GGG TGG GCG GGA TGG CTC ¢TG TCA CCC CGC GGC TCC CGG	273
20	CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGC	312 351
	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GGC CCC	429
	CTA GGG GGC GTT GCC AGG GCC CTG GCG CAT GGC GTC CGG	468
	GTT GTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT CTG	507
	CCT GGT TGC TCT TTC TCT ATC TTC CTT TTG GCT TTG CTG	546
25	TCT TGT CTG ACC ATC CCA GCT TCC GCT	573
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SEQUENCE CHARACTERISTICS: LENGTH: | 573 base pairs (A)

TYPE: nucleic acid (B) (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

ORIGINAL SOURCE: (vi)

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE:

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 124:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39 AAC ACC AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC 78 GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156 TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195 CCC AAG GCT CGC CGG CCC GAG GGT AGG GCC TGG GCT CAG 234 CCC GGG TAC CCT TGG CCC CTC TAT GGC GAC GAG GGC ATG 273 15 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCC CGG 312 CCT AAT TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT 351 AAT CTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCT CCC 429 TTA GGG GGC GTT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468 GTT CTG GAG GAC GGC GTG AAT TAC GCA ACA GGG AAT TTG 507 CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG CTG 546 TCC TGC TTG ACC ATC CCA GCT TCC GCT 573 20

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
- TOPOLOGÝ: (D) linear

(vi) ORIGINAL SOURCE:

- ORGANISM: homosapiens (A)
- (C) INDIVIDUAL ISOLATE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

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30	ATG	AGC	ACA	AAT	CCT	AAA	CCT	¢аа	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	AAC	CGT	CGC	CCA	CAG	ĠAC	GTT	AAG	TTC	CCG	GGC	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	ĠTA	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	ĠGC	GCG	ACA	AGG	AAG	ACT	156
	TCG	GAG	CGA	TCC	CAG	CCA	CGT	dGG	AGG	CGC	CAG	CCC	ATC	195
	CCC	AAA	GAT	CGG	CGC	TCC	ACT	GGC	AAG	TCC	TGG	GGA	AAA	234
	CCA	GGA	TAT	CCC	TGG	CCC	CTG	T ⁱ ΔTr	GGG	ΔΔͲ	GAG	GGD	CTC	273

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5	CCC TCC TGG GGC AAC GTG GGT AAG GCC GAC CTC ATG TTG GGT GGC GTC GTC CTG GAG GAC CCT GGT TGC TCC	TGG CTC CTG TCC CCC CGA GGT TCC CGT CCC AAT GAC CCC CGG CAT AGG TCG CGC GTC ATC GAT ACC CTA ACG TGC AGC CTT 39 GGG TAC GTC CCC GTC GTA GGC GGC CCG 42 GCC AGA GCT CTC GCG CAT GGC GTG AGA GGG GTT AAT TAT GCA ACA GGG AAC TTA TTT TCT ATT TTC TTG CTG GCC CTA CTG ATT CCA GTC TCC GCT 57	1 0 9 8 7 6
	(2) INFORMATIO	N FOR SEQ ID NO: 126:	
10		SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: US10	
15	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 126:	
20	AAC ACT AAC CGT GGC GGC CAG ATC AGG GGC CCC AGG TCG GAG CGG TCC CCC AAA GAT CGG CCA GGA TAC CCT GGC TGG GCA GGA CCC TCT TGG GGC AAC GTG GGT AAG GCC GAC CTC ATG	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAA GAC GTT AAG TTT CCG GGC GTT GGC GGA GTA TAC TTG TTG CCG CGC TTG GGT GTG CGC GCG ACA AGG AAG ACT CAG CCA CGT GGG AGG CGC CAG CCC ATC CGC CCC ACT GGC AAG TCC TGG GGA AAA TGG CCC CTA TAT GGG AAT GAG GGA CTC CCC ACT GTC CCC CGA GGT TCC CGT CCC ACT GAT CCC CGG CAT AGG TCG CGC GTC ATC GAT ACC CTA ACG TCG CGC GTC ATC GAT ACC CTA ACG TCC GGC TTT GGA TAC ATC CCC GTC GTG GGC GTC AGG GCC AGA GCT CTC GCG CAT GGC GTG AGG GGG GTT AAT TAT GCA ACA GGG AAC TTA	8 7 6 5 4 3 2 1 0 9 8
25	CCC GGT TGC TCC	TTT TCT ATC TTC TTG CTG GCC TTA CTG 54 ATT CCA GTC TCT GCT 57:	6
		ON FOR SEQ ID NO: 127: SEQUENCE CHARACTERISTICS:	
30		(A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
35	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: T9	
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	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 127:	
5	AAC ACC AAC CGT GGC GGC CAG ATC AGG GGC CCT AGG TCG GAG CGG TCC CCC AAA GAT CGG CCA GGA TAC CCC GGC TGG GCG GGA CCC TCT TGG GGC AAC GTG GGT AAG GCC GAC CTC ATG CTT GGT GGC GTT GTC CTG GAG GAC CCT GGT TGC TCT	CCA AAA CCC CAA AGA AAA ACC ATA AGA CGC CCA CAG GAC GTT AAG TTC CCG GGC GTT GGC GGA GTA TAC TTG TTG CCG CGC ACG CCA CGT GGG CGC TCC ACT GGC AGG CGC CAG CCC ATC AGG CCT CTA TAT CCC AGT GAC CCC AGT GAC CCC AGT GAC CCC AGT GAC CCC AGT GAC CCC AGT GAC CCC AGT GAC CCC CGA GGT TCC CCC CGA GGT TCC CCC CGA GGT TCC CCC AGT GAC CCC AGT GAC CCC CGG CAT AGG TCG CCC AGC CCC AGC CCC CGG CAT AGG TCG CCC AGC CCC AGC CCC CGG CAT AGG TCC CCC AGC CCC AGC CCC CGG CAT AGG TCG CCC CGG CAT AGG TCG CCC CGG CAC GGC CCC CGG CAC GGC CCC CCG CGC AGA GCT CTC CCC CGG CAC GGC CCC CCG CAC GCC CCG CCC CCG CCC CCG CCC CCG CCC CCC CCC CCC	39 78 117 156 195 234 273 312 351 390 429 468 507 546 573
15	(2) INFORMATÎ	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
20	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: T2 SEQUENCE DESCRIPTION: SEQ ID NO: 128:	
25	AAC ACT AAC CGT GGC GGC CAG ATC AGG GGC CCC AGG TCG GAG CGG TCC CCT AAA GAT CGG CCA GGA TAC CCC GGC TGG GCA GGA	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAA GAC GTT AAG TTT CCG GGC GTT GGC GGA GTA TAC TTG CTG CCG CGC TTG GGT GTG CGC GCG ACA AGG AAG ACT CAG CCT CGT GGA AGG CGC CAG CCC ATC CGC TCC ACT GGC AAG TCC TGG GGA AAA TGG CCC CTG TAT GGG AAT GAG GGG CTC TGG CTC CTG TCC CCC CGA GGT TCT CGT CCC AAT GAC CCC CGG CAT AGG TCG CGC GTC ATC GAT ACC TGC GGC TTT GGG TAC ATC CCC GTC GTA GGC GCC CCG	39 78 117 156 195 234 273 312 351 390
30	CTT GGT GGT GTC GTC CTG GAG GAC CCC GGT TGC TCC	GGG TAC ATC CCC GTC GTA GGC GCC CCG GCC AGA GCT CTT GCG CAT GGC GTG AGA GGA GTT AAT TAT GCA ACA GGT AAC TTA TTT TCT ATC TTC TTG CTA GCC CTG CTG ATT CCG GTT TCA GCT	429 468 507 546 573

INFORMATION FOR SEQ ID NO: 129:

35

(2)

		- 168 -	
0			
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: T8	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 129:	
10	AAC ACA AAC CGC GGC GGC CAG ATC AGG GGC CCT AGG TCC GAG CGA TCC CCG AAA GAT CGG	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAG GAC GTC AAG TTC CCG GGT GTT GGC GGA GTT TAC TTG CTG CCG CGC TTG GGT GTG CGC GCG ACA AGG AAG ACT CAG CCG CGT GGG AGA CGC CAG CCC ATC CGC TCC ACC GGC AAG TCC TGG GGA AAA TGG CCT CTT TAC GGA AAC GAG GGC TGC	39 78 117 156 195 234 273
15	GGT TGG GCA GGT CCT ACT TGG GGC AAT TTG GGC AGA GCC GAC CTC ATG GTC GGA GGC GTC GTC CTG GAA GAC CCT GGT TGC TCT	TGG CTC CTG TCC CCC CGC GGG TCT CGT CCC ACT GAC CCC CGG CAT AGA TCA CGT GTC ATC GAT ACC ATT ACA TGT GGT TTT GGG TAC ATC CCT GTC GTT GGC GCC CCG GCC AGA GCT CTG GCA CAT GGT GTT AGG GGG ATA AAC TAT GCA ACA GGG AAT TTG TTT TCT ATC TTC TTG CTT GCT CTT GTG CCA GTG TCT GCA	312 351 390 429 468 507 546 573
20	(2) INFORMATI	ON FOR SEQ ID NO: 130:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: US1	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 130:	
30	AAC ACA AAC CGC GGC GGT CAG ATC AGG GGC CCC AGG TCC GAG CGA TCC CCG AAA GAT CGG CCA GGA TAT CCT GGC TGG GCA GGT	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAG GAC GTC AAG TTC CCG GGT GTT GGC GGA GTT TAC TTG CTG CCG CGC TTG GGT GTG CGC GCG ACA AGG AAG ACT CAG CCG CGT GGG AGA CGC CAG CCC ATC CGC TCC ACC GGC AAG TCC TGG GGA AAG TGG CCT CTG TAC GGA AAC GAG GGC TGC TGG CTC CTG TCC CCC CGC GGG TCT CGT CCC ACT GAC CCC CGG CAC AGA TCA CGT	39 78 117 156 195 234 273 312
35		CCC ACT GAC CCC CGG CAC AGA TCA CGT	351
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5	GCC GAC CTC ATG GTC GGA GGC GTC GTC CTG GAA GAC CCT GGT TGC TCC	GTC ATC GAT ACC ATT ACG TGT GGT TTT GGG TAC ATC CCT GTC GTT GGC GCC CCG GCC AGA GCT CTG GCA CAC GGT GTT AGG GGG ATA AAT TAC GCA ACA GGG AAT CTG TTT TCT ATC TTC TTA CTT GCT CTT CTG GTG CCG GTG TCT GCA	390 429 468 507 546 573
5	(2) INFORMATION	ON FOR SEQ ID NO: 131:	
10	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: DK11	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 131:	
15	AAT ACA AAC CGC GGC GGC CAG ATC AGG GGC CCC AGG TCC GAG CGA TCC	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAG GAC GTT AAG TTC CCG GGT GTT GGC GGA GTT TAC TTG CTG CCG CGC TTG GGT GTG CGC ACG ACA AGG AAG ACT CAG CCG CGT GGG AGA CGC CAG CCC ATC CGC TCC ACC GGC AAG CCC TGG GGA AAG	39 78 117 156 195 234
20	CCA GGA TAT CCT GGC TGG GCA GGT CCT AAT TGG GGC AAT TTG GGT AAA GCC GAC CTC ATG GTC GGA GGC GTC	TGG CCC CTG TAT GGA AAC GAG GGC TGC TGG CTC CTG TCC CCC CGC GGG TCT CAT CCC ACT GAC CCC CGG CAT AAA TCA CGC GTC ATC GAC ACC ATT ACG TGT GGT TTT GGG TAC ATC CCT GTC GTC GGC GCC CCG GCC AGA GCT CTG GCA CAC GGT GTT AGA	273 312 351 390 429 468
25	CCT GGT TGC TCT TCA TGC TGC ACA	GGG ATA AAT TAC GCA ACA GGG AAT CTG TTT TCT ATC TTC TTA CTT GCT CTT CTG GTG CCA GTG TCT GCG	507 546 573
		ON FOR SEQ ID NO: 132:	
30	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
·	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SW3	
35	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 132:	
	372577_1		

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	ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAT ACA AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGT GGC GGC CAG ATC GTT GGC GGA GTT TAC TTG CTG CCG CGC	78 117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACA AGG AAG ACT TCC GAG CGA TCC CAG CCG CGT GGG AGA CGC CAG CCC ATC	156
5	CCG AAA GAT CGG CGC TCC ACC GGC AAG TCC TGG GGA AAG	195 234
J	CCA GGA TAT CCT TGG CCC CTG TAT GGA AAC GAG GGC TGC GGC TGG GCA GGT TGG CTC CTG TCC CCC CGC GGG TCT CAT	273 312
	CCT AAT TGG GGC CCC ACT GAC CCC CGG CAT AGA TCA CGC AAT TTG GGC AAA GTC ATC GAC ACC ATT ACG TGT GGT TTT	351 390
	GCC GAC CTC ATG GGG TAC ATC CCT GTC GTT GGC GCC CCG	429
	GTC GGA GGC GTC GCC AGA GCT CTG GCA CAC GGT GTT AGA GTC CTG GAA GAC GGG ATA AAT TAC GCA ACA GGG AAT CTG	468 507
10	CCT GGT TGC TCT TTT TCT ATC TTC TTA CTT GCT CTT CTG TCG TGC TTC ACA GTG CCA GTG TCT GCG	546 573
	(2) INFORMATION FOR SEQ ID NO: 133:	
	(i) SEQUENCE CHARACTERISTICS:	
1.5	(A) LENGTH: 573 base pairs (B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: DK8	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:	
	ATG'AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACA AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGT	39 78
	GGC GGC CAG ATC GTT GGC GGA GTT TAC TTG CTG CCG CGC	117
	TCC GAG CGA TCC CAG CCG CGT GGG AGG CGC CAG CCC ATC	156 195
25	CCG AAA GAT CGG CGC FCC ACC GGC AAG TCC TGG GGA AAA CCG GGA TAT CCT TGG CCC CTG TAT GGA AAC GAG GGC TGC	234 273
	GGC TGG GCA GGT TGG PTC CTG TCC CCC CGC GGG TCT CGT	312 351
	AAT TTG GGC AAA GTC ATC GAC ACC ATT ACG TGT GGT TTT	390
	GTT GGA GGC GTC GCC AGA GCT CTG GCA CAC GGT GTT AGG	429 468
30		507 546
50	TCG TGC TGC ACA GTG CA GTG TCT GCG	573
	(2) INFORMATION FOR SEQ ID NO: 134:	

SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs

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35

(i)

171 -(B) TYPE: Inucleic acid (C) STRANDEDNESS: single TOPOLOGY: linear (D) ORIGINAL SOURCE: (vi) ORGANISM: homosapiens (A) INDIVIDUAL ISOLATE: (C) 5 SEQUENCE DESCRIPTION: SEQ ID NO: 134: (xi) ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA 39 AAC ACT AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78 GGT GGC CAG ATC GTT GGC GGA GTA TAC TTG CTG CCG CGC 117 AGG GGC CCG AGA TTG GGT GTG CGC GCG ACG AGG AAA ACT TCC GAA CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC ATC 156 10 195 CCT AAA GAT CGG CGC ACC ACT GGC AAG TCC TGG GGA AGG 234 CCA GGA TAC CCT TGG CCC CTG TAT GGG AAT GAG GGC CTC 273 GGC TGG GCA GGG TGG CTC CTG TCC CCC CGC GGT TCT CGC 312 CCT TCA TGG GGC CCC ACC GAC CCC CGG CAT AAA TCG CGC 351 AAC TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGT TTT 390 GCC GAC CTC ATG GGG TAC ATA CCC GTC GTT GGC GCT CCC 429 GTT GGC GGC GTT GCC AGA GCC CTC GCC CAT GGG GTG AGG 468 15 GTT CTG GAG GAC GGG ATA AAT TAT GCA ACG GGG AAT TTG 507 CCC GGT TGC TCT TTC TCT ATC TTT CTC TTG GCC CTC TTG 546 TCT TGC ATC TCT GTG CCA GTT TCC GCC 573 INFORMATION FOR SEQ ID NO: 135: (2) SEQUENCE CHARACTERISTICS: .(i) 20 (A) LENGTH: 573 base pairs (B) TYPE: hucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (vi) ORIGINAL SOURCE: ORGANI\$M: homosapiens (A) 25 (C) INDIVIDUAL ISOLATE: HK10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135: ATG AGC ACA CTT CCT AAA CCT CAA AGA AAA ACC AAA AGA 39 AAC ACC ATC CGT CGC CCA CAG GAC GTT AAG TTC CCG GGT 78 GGC GGA CAG ATC GTT GGT GGA GTA TAC GTG TTG CCG CGC 117 AGG GGC CCA CGA TTG GGT GT\$ CGC GCG ACG CGT AAA ACT 156 30 TCT GAA CGG TCG CAG CCT CGC GGA CGA CAG CCT ATC CCC AAG GCG CGT CGG AGC GAA GGC CGG TCC TGG GCT CAG 195 234 CCC GGG TAC CCT TGG CCC CTC TAT GGT AAC GAG GGC TGC 273

GGG TGG GCA GGA TGG CTC CTG TCC CCA CGC GGC TCC CGT

CCA TCT TGG GGC CCA AAC GAC CCC CGG CGA CGG TCC CGC

AAT TTG GGT AAA GTC ATC GAT ACC CTT ACG TGC GGA TTC

GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCT CCC

312

351

390

429

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	GCC CTT GAA GAC CCC GGT TGC TCC	GCA AGA GCC CTC GCG CAT GGC GTG AGG GGG ATA AAT TTC GCA ACA GGG AAC TTG TTT TCT ATC TTC CTT CTT GCT CTG TTC CAT CCA GCA GCT AGT	468 507 546 573
5	(2) INFORMATIO	ON FOR SEQ ID NO: 136:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: \573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: S52	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 136:	
15	AAC ACC ATC CGT GGC GGA CAG ATC AGG GGC CCA CGA TCT GAA CGG TCA	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAG GAC GTT AAG TTC CCG GGT GTT GGT GGA GTA TAC GTG TTG CCG CGC TTG GGT GTG CGC GCG ACG CGT AAA ACT CAG CCT CGC GGA CGA CGA CAG CCT ATC	39 78 117 156 195
20	CCC GGG TAC CCT GGG TGG GCA GGG CCA TCT TGG GGC AAT TTG GGT AAA GCC GAC CTC ATG GTA GGA GGC GTC GCC CTT GAA GAC CCC GGT TGC TCC	CGG AGC GAA GGC CGG TCC TGG GCT CAG TGG CCC CTC TAT GGT AAT GAG GGC TGC TGG CTC CTG TCC CCA CGC GGC TCC CGT CCA AAC GAC CCC CGG CGG AGG TCC CGC GTC ATC GAT ACC CTT ACG TGC GGA TTC GGG TAC ATC CCG CTC GTC GGC GCT CCC GCA AGA GCC CTC GCG CAT GGC GTG AGG GGG ATA AAT TTT GCA ACA GGG AAC TTG TTT TCT ATC TTC CTT CTT GCT CTG TTC CAT CCT GCA GCT AGT	234 273 312 351 390 429 468 507 546 573
25	(2) INFORMATIO	ON FOR SEQ ID NO: 137:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	•
30	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: S2	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 137:	
35	ATG AGC ACA CTT	CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	372577_1		

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AAC ACC ATC CGT CGC CCA CAG GAC ATC AAG TTC CCG GGT
                                                                 78
     GGC GGA CAG ATC GTT GGT GGA GTA TAC GTG TTG CCG CGC
                                                                117
     AGG GGC CCA CGA TTG GGT GTG CGC GCG ACG CGT AAA ACT
                                                                156
     TCT GAA CGG TCA CAG CCT CGC GGA CGG CGA CAG CCT ATC
     CCC AAG GCG CGT CGG AGC GAA GGC CGA TCC TGG GCT CAG
                                                                234
     CCC GGG TAC CCT TGG CCC CTC TAT GGT AAC GAG GGC TGC
                                                                273
     GGG TGG GCA GGG TGG CTC CTG
                                  TCC CCA CGC GGC TCC CGT
                                                                312
 5
                                  CCC CGG CGG AGG TCC CGC
     CCA TCT TGG GGC CCA AAT GAC
                                                                351
     AAT TTG GGT AAA GTC ATC GAT
                                  ACC CTT ACG TGC GGC TTC
                                                                390
     GCC GAC CTC ATG GGG TAC ATC
                                  CCG CTC GTC GGC GCT CCC
                                                                429
     GTA GGA GGC GTC GCA AGA GCC
                                  CTC GCG CAT GGC GTG AGG
                                  TTT GCA ACA GGG AAC TTG
     GCC CTT GAA GAC GGG ATA AAT
                                                                507
     CCC GGT TGC TCT TTT TCT ATC TTC CTT CTT GCC CTG TTC
                                                                546
     TCT TGC TTA ATT CAT CCA GCA GCT AGT
                                                                573
10
      (2)
            INFORMATION FOR SEQ ID NO: 138:
                      SEQUENCE CHARACTERISTICS:
             (i)
                           LENGTH: | 573 base pairs
                      (A)
                           TYPE: hucleic acid
                      (B)
                           STRANDEDNESS: single
                      (C)
                           TOPOLOGY:
                      (D)
                                      linear
15
             (vi)
                      ORIGINAL SOURCE:
                      (A)
                           ORGANISM: homosapiens
                      (C)
                           INDIVIDUAL ISOLATE:
             (xi)
                      SEQUENCE DESCRIPTION: SEQ ID NO: 138:
     ATG AGC ACA CTT CCT AAA CCT CAA AGA AAA ACC AAA AGA
                                                                 39
20
     AAC ACC ATC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT
                                                                 78
     GGC GGA CAG ATC GTT GGT GGA GTA TAC GTG TTG CCG CGC
                                                                117
     AGG GGC CCA CGA TTG GGT GTG CGC GCG ACG CGT AAA ACT
                                                                156
     TCT GAA CGG TCA CAG CCT CGC GGA CGG CGA CAG CCT ATC
                                                                195
     CCC AAG GCG CGT CGG AGC GAA GGC CGG TCC TGG GCT CAG
                                                                234
     CCT GGG TAC CCT TGG CCC CTC TAT GGT AAC GAG GGC TGC
                                                                273
     GGG TGG GCA GGG TGG CTC CTG
                                  TCC CCA CGC GGC TCC CGT
                                                                312
25
     CCA TCT TGG GGC CCA AAC GAC
                                  CCC CGG CGG AGG TCC CGC
                                                                351
     AAT TTG GGT AAG GTC ATC GAT ACC CTC ACG TGC GGA TTC
                                                                390
     GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCT CCT
                                                                429
     GTA GGG GGC GTC GCA AGA GCC CTC GCG CAT GGC GTG AGG
                                                                468
     GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAC TTG
                                                                507
     CCC GGT TGC TCC TTT TCT ATC
                                  TTC CTT CTT GCT CTG TTC
                                                                546
                                  GCT AGT
     TCT TGC CTA ATT CAT CCA GCA
                                                                573
30
     (2)
            INFORMATION FOR SEQ ID NO: 139:
             (i)
                      SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH: 573 base pairs
                           TYPE: | nucleic acid
                      (B)
                      (C)
                           STRANDEDNESS: single
35
     372577_1
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O	(D) TO	POLOGY: linear
	(A) OR	L SOURCE: GANISM: homosapiens DIVIDUAL ISOLATE: Z4
5	(xi) SEQUENC	E DESCRIPTION: SEQ ID NO: 139:
10	AAC ACC AAC CGC CGC CCC GGT GGC CAG ATC GTT GGC AGG GGC CCC AGG TTG GGT TCG GAG CGG TCG CAA CCT CCC AAG GCG CGC CAG CCA CCC GGG TAC CCT TGG CCC GGG TGG GCA GGG TGG CTC CCA TCT TGG GGC CCA AAT AAT CTG GGT AAG GTC ATC GCC GAC CTC ATG GGA TAC GTG GGG GGC GTC GCC AGG	CCT CAA AGA AAA ACC AAA CGT 78 ATG GAC GTA AAG TTC CCG GGT 78 GGA GTT TAC TTG TTG CCG CGC 117 GTG CGC GCG ACT CGA AAG ACT 156 CGT GGC AGG CGT CAA CCT ATC 195 GAG GGC AGA TCC TGG GCG CAG 234 CTC TAT GGC AAT GAG GGC TGC 273 CTG TCT CCT CGC GGC TCT CGG 312 GAT CCC CGG CGG AGA TCG CGC 351 GAT ACC CTG ACG TGC GGC TTC 390 ATC CCG ATC GTG GGC GCC CCC 429 GCT CTG GCG CAT GGC GTC AGG 468 AAC TAT GCA ACA GGG AAT CTT 507
15	CCC GGT TGC TCT TTC TCT TCG TGC CTC ACT GTT CCA	AT¢ TTC CTT TTG GCA CTT CTT 546
20	(A) LE (B) TY (C) ST	E CHARACTERISTICS: NGTH: 573 base pairs PE: nucleic acid RANDEDNESS: single
	(vi) ORIGINA (A) OR	POLOGY: linear L SOURCE: GANISM: homosapiens DIVIDUAL ISOLATE: Z8
25	(xi) SEQUENC	E DESCRIPTION: SEQ ID NO: 140:
30	AAC ACC AAC CGC CGC CCT GGC GGC CAG ATC GTT GGC AGG GGC CCC AGG TTG GGT TCG GAG CGG TCG CAA CCT CCC AAG GCA CGT CGG TCC CCC GGG TAC CCA TGG CCT GGG TGG GCA GGT TGG CTC CCG TCT TGG GGC CCA AAT AAT TTG GGT AAG GTC ATC GCC GAC CTC ATG GGA TAC GTA GGA GGC GTC GCC AGA	CCT CAA AGA AAA ACC AAA CGT 39 ATG GAT GTA AAA TTC CCA GGC 78 GGA GTT TAC TTG TTG CCG CGC 117 GTG CGC GCG ACT CGG AAG ACT 156 CGT GGC AGG CGT CAG CCT ATC 195 GAG GGT AGG TCC TGG GCT CAG 234 CTT TAC GGT AAT GAA GGC TGT 273 CTG TCC CCC CGC GGC TCT CGA 312 GAT CCC CGG CGG AGG TCG CGC 351 GAT ACC CTC ACG TGC GGC TTC 390 ATC CCG CTC GTG GGC GCC CCA 429 GCC CTG GCG CAT GGC GTC AGG 468
35		AAC TAT GCA ACA GGG AAC CTT 507
	272577 1	

o	CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCA CTT CTC TCG TGC CTA ACC GTC CCA GCG TCT GCT	546 573
	(2) INFORMATION FOR SEQ ID NO: 141:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: Z1	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:	٠
15	ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC CGT CGC CCC ATG GAT GTG AAA TTC CCG GGC GGC GGC GGC CAG ATC GTT GGC GGA GTT TAC TTG CTG CCG CGC AGG GGC CCC CGG TTG GGT GTC CGC GCA GCT CGG AAG ACT TCG GAG CGC TCAA CCT CGT GGC AGG CGT CAG CCT ATC CCC AAG GCG CGC CGG TCC GAG GGC AGG TCC TGG GCT CAG CCC AAG GCG CGC CGC TCC GAG GGC AAT GAG GGC TGT CCC GGG TAC CCT TGG CCC CTT TAC GGC AAT GAG GGC TGT GGG TGG GCA GGG TCC CGG GGT TCC AGG CCG TCT TGG GCC CCC CGC GGT TCC AGG CCG TCT TGG GCC CCC CGC GGT TCC AGG CCG TCT TGG GGC CCC AAT GAT CCC CGG CGT AGG TCC CGT AAT CTG GGT AAA GTC ATC GAT ACC CTG ACG TGT GGC TTC GCC GAC CTC ATG GGA TAC ATT CCG CTC GTA GGC GCC CCT GTG GGT GGC GTC AGG GCC CTT GTG GGT GGC GTC AGG GCC CTT CTC GTG GGT GGC GTC AGG GCC CTT CTC TTC TTC TTC TTT CTT CTT C	39 78 117 156 195 234 273 312 351 390 429 468 507 546 573
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: Z5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:	
35	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC CGC CGC CCC GGT GGT CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT	39 78 117 156

0		
5	TCG GAG CGG TCG CAA CCT CGC GGC AGG CGT CAG CCT ATC CCC CAG GCA CGT CGG TCC GAG GGC AGG TCC TGG GCT CAG CCC GGG TAC CCT TGG CCT CTT TAT GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG CTC CTG TCC CCC CGC GGA TCT CGG CCA TCT TGG GGC CAA AAT GAT CCC CGG CGT AGG TCC CGC AAT CTG GGT AAG GTC ATC GAT ACC CTG ACG TGT GGC TTC GCC GAC CTC ATG GGA TAC ATT CCC CTC GTC GGC GCC CCA GTA GGT GGC GTC AGG GCC CTG GGC GTC AGG GCC CTG GGC GTC AGG GCC CTG GGC GTC AGG GCC CTG GGC GTC AGG GCC CTG GGC GTC AGG GCC CTG GGC GTC AGG GCC CTG GGC GTC AGG GCC CTG GGC GTC AGG GCC CTG GGT TGC TCC TTT TCT ATC TTC CTA CTT GCA CTT TTC TCG TGC TGC TTG ACA ACA CCG GCA TCC GCT	195 234 273 312 351 390 429 468 507 546 573
	(2) INFORMATION FOR SEQ ID NO: 143:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: Z6	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:	
20	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC CGC CGC CCC ATG GAC GTT AAG TTC CCG GGT GGT GGC CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGA CGC CAG CCT ATC CCC AAG GCA CGT CGA TCT GAG GGA AGG TCC TGG GCT CAG CCC GGG TAT CCA TGG CCT CTT TAC GGT AAT GAG GGT TGC GGG TGG GCG TGG CTC CTG TCA CCC CGT GGC TCT CGA	39 78 117 156 195 234 273 312
25	CCG TCT TGG GGT CCA AAT GAT CCC CGG CGA AGG TCC CGC AAC TTG GGT AAG GTC ATC GAT ACT CTA ACT TGC GGT TTC GCC GAT CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC CCC GTG GGC GGC GTC GCC AGG GCC CTG GCA CAT GGT GTT AGG GCT GTG GAG GAC GGG ATC AAT TAT GCA ACA GGG AAT CTT CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTA ACT GTT CCC ACC TCG GCC	351 390 429 468 507 546 573
	(2) INFORMATION FOR SEQ ID NO: 144:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
35	(vi) ORIGINAL SOURCE:	
	372577_1	

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ORGANISM:
                         (A)
                                          homosapiens
                         (C)
                              INDIVIDUAL ISOLATE:
                        SEQUENCE DESCRIPTION: SEO ID NO: 144:
              (xi)
      ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT
                                                                        39
      AAC ACC AAC CGC CGC CCC ATG GAC GTT AAG TTC CCG GGC
                                                                        78
 5
      GGT GGC CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC AGA TTG GGT GTG CGC ACA ACT AGG AAG ACT
                                                                       117
                                                                       156
      TCG GAG CGG TCG CAA CCT CGT GGG AGA CGT CAG CCT ATC
                                                                       195
      CCC AAG GCA CGT CGA TCT GAG GGA AGG TCC TGG GCT CAA
                                                                       234
      CCC GGG TAC CCA TGG CCT CTT TAC GGT AAC GAG GGT TGC
                                                                       273
      GGG TGG GCA GGA TGG CTC TTG TCA CCC CGT GGC TCT CGA
                                                                       312
      CCG TCT TGG GGC CCA AAT GAT CCC CGG CGA AGG TCC CGC AAC TTG GGT AAG GTC ATC GAT ACC CTA ACC TGC GGC TTT GCC GAC CTC ATG GGA TAC AT¢ CCG CTC GTA GGC GCC CCC
                                                                       351
                                                                       390
10
                                                                      429
      GTG GGC GGC GTC GCC AGG GCC CTA GCG CAT GGC GTT AGG
                                                                      468
      GCT CTG GAG GAC GGG ATT AAT TAT GCA ACA GGG AAC CTT
                                                                       507
      CCC GGT TGC TCT TTT TCT ATC TTC CTC TTG GCA CTT CTT
                                                                       546
      TCG TGC CTG ACT GTT CCC GCC TCG GCC
                                                                       573
15
             INFORMATION FOR SEQ ID NO: 145:
      (2)
                        SEQUENCE CHARACTERISTICS:
              (i)
                        (A)
                              LENGTH: 573 base pairs
                        (B)
                              TYPE: nucleic acid
                        (C)
                              STRANDEDNESS: single
                              TOPOLOGY: linear
                        (D)
20
              (vi)
                        ORIGINAL SOURCE:
                        (A)
                              ORGANISM: homosapiens
                              INDIVIDUAL ISOLATE:
                        (C)
              (xi)
                        SEQUENCE DESCRIPTION: SEQ ID NO: 145:
      ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC CGC CCA ATG GAC GTT AAG TTC CCG GGT
                                                                        39
25
                                                                        78
      GGC GGC CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC
                                                                       117
      AGG GGC CCT AGA TTG GGT GTG CGC GCG ACT AGG AAG ACT
      TCG GAG CGG TCG CAA CCT CGT GGG AGG CGC CAG CCT ATC
                                                                       195
      CCC AAG GCG CGC CAA CTC GAG GGT AGG TCC TGG GCT CAG
                                                                       234
      CCT GGG TAT CCT TGG CCC CTT TAC GGC AAT GAG GGC TGC
                                                                       273
      GGG TGG GCG GGA TGG CTC CTG TCA CCC CGT GGC TCT CGG
                                                                       312
      CCG TCT TGG GGC CCG AAT GAT CCC CGG CGG AGG TCC CGC
                                                                       351
30
      AAC TTG GGT AAG GTC ATC GAT ACC CTA ACT TGC GGC TTC
                                                                       390
      GCC GAC CTC ATG GGA TAC ATC CCG GTC GTA GGC GCC CCC
                                                                       429
      GTG GGT GGC GTC GCC AGA GCC CTG GCG CAT GGC GTC AGG
                                                                       468
      CTT CTG GAG GAC GGG GTC AAT TAT GCA ACA GGG AAT CTT
                                                                       507
      CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCA CTG CTC
                                                                       546
      TCG TGC CTG ACT GTT CCC GCT TCG GCC
                                                                       573
35
```

0			
	(2) INFORMATI	ON FOR SEQ ID NO: 146:	
5	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA4	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 146:	
10	AAC ACC AAC CGC	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAG GAC GTT AAG TTC CCG GGC GTT GGT GGA GTC TAC TTG TTG CCG CGC	39 78 117
15	AGG GGC CCT AGG TCA GAA CGG TCG CCC AAG GCG CCC GGG TAC CCT GGG TGG GCA GGG CCT AAT TGG GGC AAT TTG GGT AAG GCC GAC CTC ATG GTT GGG GGC GTC GTT CTT GAG GAC	TTG GGT GTG ¢GC GCG ACT CGG AAG ACT CAA CCC CGT ¢GG CGG CGC CAG CCT ATT CAA CCC ACG ¢GC CGG TCC TGG GGT CAA TGG CCC CTT TAC GCC AAT GAG GGC CTC TGG TTG CTC TCC CCC CGA GGC TCT CGG CCC AAT GAC CCC CGG CGA AAG TCG CGC GTC ATC GAT ACC CTA ACG TGC GGA TTC GGG TAC ATC CCG CTC GTA GGC GGC CCC GCA AGG GCC CTT GCA CAT GGT GTG AGG GGG GTA AAC TAT GCA ACG GGG AAT TTG TTC TCT ATC TTT ATC CTT GCA CTT CTC	156 195 234 273 312 351 390 429 468 507 546
20		GTC CCG GCC TCT GCA	573
	(2) INFORMATI	ON FOR SEQ ID NO: 147:	
25	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA5	
30	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 147:	
	AAC ACC AAC CGC GGT GGT CAG ATC AGG GGC CCT AGA TCA GAA CGG TCG	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAG GAC GTC AAG TTC CCG GGC GTT GGT GGA GTT TAC TTG TTG CCG CGC TTG GGT GTG CGC GCG ACT CGG AAG ACT CAA CCC CGT GGG CGC CAG CCT ATT CAA CCC ACG GGC CGG TCC TGG GGT CAA	39 78 117 156 195 234
35	372577 1		

0		1	
5	GGG TGG GCA GGG CCT AAT TGG GGC AAT TTG GGT AAG GCC GAC CTC ATG GTT GGG GGC GTC GTT CTT GAG GAC CCC GGT TGC TCT	TGG CCC CTT TAC GCC AAT GAG GGC CTC TGG TTG CTC TCC CCC CGA GGC TCT CGG CCC AAT GAC CCC CGG CGA AAA TCG CGC GTC ATC GAT ACC CTA ACG TGC GGA TTC GGG TAC ATC CCG CTC GTA GGC GGC CCC GCA AGG GCC CTC GCA CAT GGT GTG AGG GGG GTA AAC TAT GCA ACA GGG AAT TTG TTC TCT ATC TTT ATC CTT GCA CTT CTC GTC CCA GCC TCT GCA	273 312 351 390 429 468 507 546 573
	(2) INFORMATIO	N FOR SEQ ID NO: 148:	
10		SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA7	
15	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 148:	
20	AAC ACC AAC CGC GGT GGT CAG ATC GAG GGC CCT AGG TCA GAA CGG TCG CCC AAG GCG CCC GGG TAC CCT GGG TGG GCA GGG CCT AAT TGG GGC GCC GAC CTC ATG GGC AAC CTC ATG GGC GAC CTC ATG GGC GAC CTC ATG GGC GAC CTC ATG GGT AAC CTC ATG GGT AAC CTC ATG GGC GAC CTC ATG GGC GAC CTC ATG GGC GAC CTC ATG GGT AAC CTC ATG ATG ATG ATG ATG ATG ATG ATG ATG ATG	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAG GAC GTC AAG TTC CCG GGC GTT GGT GGA GTT TAC TTG TTG CCG CGC TTG GGT GTG CGC GCG ACT CGG AAG ACT CAA CCC CGT GGG CGC CAG CCT ATT CAA CCC ACG GGC CGG TCC TGG GGT CAA TGG CCC CTT TAC GCC AAT GAG GGC CTC TGG TTG CTC TCC CCC CGA GGC TCT CGG CCC AAT GAC CCC CGG CGA AAG TCG CGC GTC ATC GAC ACC CTA ACA TGC GGA TTC GGG TAC ATC CCG CTC GTA GGC GGC CCC GCA AGG GCT CTC GCA AGG GCC CCC GCA AGG GCT CTC GTA GGC GGC CCC GCA AGG GCT CTC GCA CAC GGT GTG AGG	39 78 117 156 195 234 273 312 351 390 429 468
25	GTT CTT GAG GAC (CCC GGT TGC TCT	GGG GTA AAT TAC GCA ACA GGG AAT CTG TTC TCT ATC TTT ATC CTT GCA CTT CTC GTC CCA GCC TCC GCA	507 546 573
	(2) INFORMATION	N FOR SEQ ID NO: 149:	
30		SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA1	
35			

0		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:	
5	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC AAC CTC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC AGG TCG CAA CCC CGT GGG CGC CAG CCT ATT CCC AAG GCG CGC CAA CCC CGT GGG CGG CGC CAG CCT ATT CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA CCC GGG TGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG TGG TGG CCC CTT TAC GCC CCC CGA GGC TCT CGG CCT AAT TTG GGT AAG GCC CCC CGG CGG AAG TCG CGC CCC AAT TTG GGT AAG GCC CCC CTT ACC CCC CGG CGG AAG TCG CGC CCC AAT TTG GGT AAG GCC CCC CTT ACC CCC CGG CGG AAG TCC CCC CGC CGC CGC CGC CCC CGC CGC CCC CCC CGC CGC CCC CCC CCC CGC CCC 39 78 117 156 195 234 273 312 351 390	
10	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTT CTT GAG GAC GGG GTA AAC TAC GCA ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTT TCC TGT CTG ATC ATC CCG GCC TCT GCA	429 468 507 546 573
	(2) INFORMATION FOR SEQ ID NO: 150:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA3	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:	
25	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC AAC CGC CG	39 78 117 156 195 234 273 312 351 390 429 468 507 546 573
	(2) INFORMATION FOR SEQ ID NO: 151:	

		- 181 -	
٥	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA13	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 151:	
10	AAC ACC AAC CGC GGT GGT CAG ATC AGG GGC CCT AGG TCA GAA CGG TCG CCC AAG GCG CGC	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAG GAC GTC AAG TTC CCG GGC GTT GGT GGA GTT TAC TTG TTG CCG CGC TTG GGT GTG CGC GCA ACT CGG AAG ACT CAA CCC CGT GGA CGG CGT CAG CCT ATC CAG CCC ACG GGC CGG TCC TGG GGT CAA	39 78 117 156 195 234
15	GGG TGG GCA GGG CCT AAT TGG GGC AAC TTG GGT AAG GCC GAC CTC ATG GTT GGG GGC GTC GTC CTT GAG GAC CCC GGT TGC TCT	TGG CCC CTT TAT GCC AAT GAG GGC CTC TGG TTG CTC TCC CCC CGA GGC TCT CGG CCC AAT GAC CCC CGG CGG AAA TCG CGC GTC ATC GAT ACC CTG ACG TGC GGA TTC GGG TAC ATC CCG CTC GTA GGC GGC CCC GCA AGG GCT CTC GCA CAC GGT GTG AGG GGG GTA AAC TAT GCA ACA GGG AAT TTA TTC TCT ATC TTT ATC CTT GCA CTT CTT GTC CCG ACC TCT GCC	273 312 351 390 429 468 507 546 573
20	(2) INFORMATION	ON FOR SEQ ID NO: 152:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA6	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 152:	
30	AAC ACC AAC CGC GGT GGT CAG ATC AGG GGC CCT CGT TCG GAA CGG TCG CCC AAG GCG CGC CCC GGG TAC CCT GGG TGG GCA GGG	CCT AAA CCT CAA AGA AAA ACC CAA AGA CGC CCA CAG GAC GTC AAG TTC CCG GGC GTT GGT GGA GTT TAC TTG TTG CCG CGC ATG GGT GTG CAA CCC CGT GGA CGG CGT CAG CCT ATT CAA TCC GCG GGT CGG TCC TGG GGT CAA TGG CCC CTT TAC GCC AAT GAG GGC CTC TGG TTG CTC TCC CCC CGA GGC TCT CGG CCC AAT GAC CCC CGC	39 78 117 156 195 234 273 312 351
35	372577_1		
		· ·	

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	GCC GAC CTC ATG GTT GGG GGC GTC GTT CTT GAG GAC CCC GGT TGC TCT	GTC ATC GAT ACC CTA ACG TGC GGA TTC GGG TAC ATC CCG CTC GTA GGC GGC CCC GCA AGG GCT CTC GCA CAC GGT GTG AGG GGG GTA AAC TAT GCA ACA GGG AAT TTG TTC TCT ATC TTT GTC CTT GCA CTT CTC GTC CCT GCC TCT GCA	390 429 468 507 546 573									
5	(2) INFORMATION FOR SEQ ID NO: 153:											
10	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear										
10	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA11										
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 153:										
15	AAC ACC AAC CGC GGT GGT CAG ATC	CCT AAA CCT CAA AGA AAA ACC AAA AGA CGC CCA CAG GAC GTC AAG TTC CCG GGC GTT GGT GGA GTT TAC TTG TTG CCG CGC TTG GGT GTG CGG GCG ACT CGG AAG ACT	39 78 117 156									
20	TCA GAA CGG TCG CCC AAG GCG CGC CCC GGG TAC CCT GGG TGG GCA GGG CCT AAC TGG GGC AAT TTG GGC AAG GCC GAC CTC ATG GTT GGG GGC GTC GCT CTT GAG GAC CCC GGT TGC TCT	CAA CCC CGT GGG CGG CGT CAG CCT ATT CAA CCC ACG GGC CGG TCC TGG GGT CAA TGG CCC TTT TAC GCC AAT GAG GGC CTC TGG CTG CTC TCC CCT CGA GGC TCT CGG CCC AAT GAC CCC CGG CGA AGA TCG CGC GTC ATC GAT ACC CTA ACG TGC GGA TTC GGG TAC ATC CCG CTC GTA GGC GGC CCC GCA AGG GCC CTC GCA CAC GGT GTG AGA GGG GTA AAT TAT GCA ACA GGG AAT CTT TTC TCC ATC TTT ATC CTT GCA CTT CTC GTC CCG GCC ACT GCA	195 234 273 312 351 390 429 468 507 546 573									
25	(2) INFORMATION	ON FOR SEQ ID NO: 154:										
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear										
30	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: HK2										
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 154:										
35	ATG AGC ACA CTT	CCA AAA CCC CAA AGA AAA ACC AAA AGA	39									
	372577_1											

0														
5	GGC GG AGG GG CCA AA CCC GG GGG TC CCA CA AAT TT GCC GA TTG GC GCA AT CCC GC	CC AAC GT CAG GC CCC AG CGA AG GCG GA TAC GG GCA AT TGG IG GGT AT CTC GC GGC IC GAG GT TGC GC CTC INFORN	ATC CGG TCC CGC CCT GGT GGC AAG ATG GTC GAC TCT ACA	GTT TTG CAG CAG TGG CCC GTC GGG GCG GCG GCG ACG	GGC GGT CCC CCT CTC AAT ATC TAC GCT ATC TCT CCA	GGA GTGA GATT GATT GATT GATT GATT GATT	GTT CGC GGC TAT TCC CCC ACC CTC TAT TTC TCG	TAC GCG AGG GGA CCC CGG CTA GCA GCA CTT GCT	TTG ACG CGC CAC AAC CGC CGT ACG GTG CAT ACA TTG	TTG AGA CAA TGG GAG GGC CGA TGT GGC GGC GGG	CCG AAG CCT GCT GGC TCC GGG GCG GCG GTG AAT	CGC ACT ATA CAG TGT CGG CGG TTC CCT AGG CTC		78 117 156 195 234 273 312 351 390 429 468 507 546 573
15	(2)	(i) (vi)	MII	SEQU (A) (B) (C) (D)	JENCI LEI TYI STI	E CHA NGTH PE: RANDI POLOG	ARACT : 19 amir EDNES	reris 91 ar no ac 38: unkr	STICS mino cid unkr	acio	ds			
20	Met Se	(xi) er Thr		(A) (C) SEQU	ORC INI JENCI	ANIS DIVII E DES	SM: DUAL SCRIE	homo ISOI TIOI		EEQ			155 : Asn	
	Thr As 15 Gln II	sn Arg Le Val	Gly	Pro Gly	20 Val	Tyr 35	Leu	Leu	Phe Pro	25 Arg	Arg	Gly	Pro	
25	Gln Pr	eu Gly 45 co Arg	Gly 60	Arg	Arg	Gln	50 Pro	Ile 65	Pro	Lys	Ala	55 Arg	Arg 70	
		yr Gly		75	1				80	_		~		
30	10	o Arg				105			_	Pro	Thr 110	Asp Thr		
		115 /s Gly	Phe				120	Gly				125	Val	
25	Gly Al	la Pro	130 Leu	Gly 145	Gly	Ala	Ala	135 Arg	Ala 150	Leu	Ala	His	140 Gly	
35					1									

Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 155

Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 170

Ser Cys Leu Thr Val Pro Ala Ser Ala 185

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- (2) INFORMATION FOR SEQ ID NO: 156:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANI\$M: homosapiens
 - (C) INDIVIDUAL ISOLATE: US11
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:
- - Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 - Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 - Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 130 135 140
- Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145
 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 - 0 Val Arg val Leu Glu Asp Gly val Ash Tyr Ala Thr Gly Ash 155 160 | 165 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 - 170 175 180
 Ser Cvs Leu Thr Val Pro Ala Ser Ala
 - Ser Cys Leu Thr Val Pro Ala Ser Ala 185 190

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	(2)	II	NFOR)ITAN	ON FOR SEQ ID NO: 157:											
5			(i)		SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 amino acids (B) TYPE: \amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown											
			(vi)		ORI((A) (C)	,										
			(xi)		SEQUENCE DESCRIPTION: S							SEQ ID NO: 157:				
10	Met 1	Ser	Thr	Asn	Pro 5	Lys	Pro	Gln	Arg	Lys 10	Thr	Lys	Arg	Asn		
	_	Asn	Arg	Arg	_	Gln 20	Asp	Val	Lys		Pro 25	Gly	Gly	Gly		
		Ile 30	Val	Gly	Gly		Tyr 35	Leu	Leu	Pro		Arg 40	Gly	Pro		
1.5			45				Thr	50					55			
15				60		_	Gln		65		_		_	70		
			_	_	75	_	Ala			80	_		_			
	Leu 85	Tyr	Gly	Asn	Glu	Gly 90	Су\$	Gly	Trp	Ala	Gly 95	Trp	Leu	Leu		
20		100		_		_	Prb 105		_	_		110	_			
		_	115				Leu	120	_			_	125			
				130			Leu		135	_				140		
					145	_	Ala		_	150				_		
25	155					160	Gly				165					
		170	_	_			Ser 175			Leu	Leu	Ala 180	Leu	Leu		
	Ser	Cys	Leu 185	Thr	Val	Pro	Ala	Ser 190	Ala							
30	(2)	II	NFORI	ITAN	ON FO	OR SI		ONO:	: 15	58:						
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown															

0 (vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158: Met Ser Thr Asn Pro Lys Pro Glh Arg Lys Thr Lys Arg Asn 5 10 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg 10 65 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro 100 105 110 15 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 135 130 Gly Ala Pro Leu Gly Gly Ala Ala| Arg Ala Leu Ala His Gly 145 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 155 160 20 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 175 Ser Cys Leu Thr Val Pro Ala Ser Ala 185 190 (2) INFORMATION FOR SEQ ID NO: 25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 amino acids (B) amino acid TYPE: (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown (vi) ORIGINAL SOURCE: 30 (A) ORGANISM: | homosapiens (C) INDIVIDUAL ISOLATE: SEQUENCE DESCRIPTION: SEQ ID NO: (xi) Met Ser Thr Asn Pro Lys Pro Gli Arg Lys Thr Lys Arg Asn 1 35 372577_1

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Thr Asn Arg Arg Pro Gln Asp Ÿal Lys Phe Pro Gly Gly Gly
     Gln Ile Val Gly Gly Val Tyr Ļeu Leu Pro Arg Arg Gly Pro
          30
                               35
     Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
                                   50
     Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
5
                   60
                                       65
     Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
                       75
                                           80
     Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
     Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
         100
                              105
10
     Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
             115
                                  120
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                  130
                                      135
     Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
                      145
                                           150
     Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
                          160
                                               165
15
     Leu Pro Gly Cys Ser Phe Ser/Ile Phe Leu Leu Ala Leu Leu
                              175
     Ser Cys Leu Thr Val Pro Ala Ser Ala
             185
                                  190
     (2)
           INFORMATION FOR SEQ ID NO:
20
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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown
- (vi) ORIGINAL \$OURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: DR4
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

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Pro Glu Gly Arg Thr Trp Ala Glm Pro Gly Tyr Pro Trp Pro
                       75
                                            80
     Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
     Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
                              105
     Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
5
             115
                                  120
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                                      135
     Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
                      145
                                           150
     Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
                          160
                                               165
10
     Leu Pro Gly Cys Ser Phe Ser | Ile Phe Leu Leu Ala Leu Leu
         170
                              175
     Ser Cys Leu Thr Val Pro Ala Ser Ala
             185
                                  190
     (2)
           INFORMATION FOR SEQ ID NO:
                                        161:
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15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 10 Thr Asn Arg Arg Pro Gln/Asp Val Lys Phe Pro Gly Gly Gly 25 20 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Ard Gln Pro Ile Pro Lys Ala Arg Gln 65 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro 30 75 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro 105 110 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120

35

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 130 135 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly 150 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 160 Leu Pro Gly Cys Pro Phe Ser Ile Phe Leu Leu Ala Leu Leu 5 170 175 Ser Cys Leu Thr Ile Pro Ala Ser Ala 185 (2) INFORMATION FOR SEQ ID NO: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown TOPOLOGY: (D) unknown ORIGINAL SOURCE: (vi) ORGANISM: homosapiens (A) 15 (C) INDIVIDUAL ISOLATE: S45 (xi) SEQUENCE DESCRIPTION: SEO ID NO: Met Ser Thr Asn Pro Lys Pro Gln Arg Ala Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 25 20 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 30 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 Gln Pro Arg Gly Arg Arg \$\psi\$ln Pro Ile Pro Lys Ala Arg Arg 65 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly His Pro Trp Pro 25 75 80 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu 90 95 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro 105 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120 125 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 30 130 135 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly 145 150 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 160 165 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 170 175 180 35 372577 1

```
190 -
     Ser Cys Leu Thr Ile Pro Ala Ser Ala
                                   1/90
              185
          INFORMATION FOR SEQ ID NO:
      (2)
                                         163:
             (i)
                      SEQUENCE CHARACTERISTICS:
 5
                            LENGTH:
                       (A)
                                    191 amino acids
                       (B)
                            TYPE:
                                   amino acid
                       (C)
                            STRANDEDNESS:
                                           unknown
                       (D)
                            TOPOLOGY: unknown
             (vi)
                      ORIGINAL SOURCE:
                       (A)
                            ORGANISM:
                                       homosapiens
                       (C)
                            INDIVIDUAL ISOLATE:
10
             (xi)
                      SEQUENCE DESCRIPTION:
                                               SEQ ID NO:
                                                            163:
     Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
     Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
                            20
                                                 25
15
     Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
           30
                                35
     Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
                                    50
     Gln Pro Arg Gly Arg Arg/Gln Pro Ile Pro Lys Ala Arg Arg
                   60
     Pro Glu Gly Arg Ala Trø Ala Gln Pro Gly Tyr Pro Trp Pro
                                             80
20
     Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
     Ser Pro Arg Gly Ser Ang Pro Ser Trp Gly Pro Thr Asp Pro
          100
                               105
     Arg Arg Arg Ser Arg A$n Leu Gly Lys Val Ile Asp Thr Leu
              115
                                   120
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
25
                  130
                                       135
     Gly Ala Pro Leu Gly Gly Ala Ala Arq Ala Leu Ala His Gly
                      145
                                            150
     Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
     155
                           160
                                                165
     Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
                               175
     Ser Cys Leu Thr Ile Pro Ala Ser Ala
30
              185
                                   190
      (2)
            INFORMATION FOR SEQ ID NO:
             (i)
                      SEQUENCE CHARACTERISTICS:
                       (A)
                            LENGTH:
                                     191 amino acids
35
     372577_1
```

amino acid

unknown

US6

110

STRANDEDNESS: unknown

ORGANISM! homosapiens

INDIVIDUAL ISOLATE:

TYPE:

ORIGINAL SOURCE:

TOPOLOGY:

(B)

(C)

(D)

(A)

(C)

(vi)

```
(xi)
                                SEQUENCE DESCRIPTION:
                                                        SEQ ID NO:
               Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
                                                      10
               Thr Asn Arg Arg Pro Gln Asp Wal Lys Phe Pro Gly Gly Gly
                                     20
                                                          25
          10
               Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
                                         35
               Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
                                             50
               Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
                                                  65
               Pro Glu Gly Arg Ala Trp Ala $\frac{1}{2}\ln Pro Gly Tyr Pro Trp Pro
                                 75
                                                      80
          15
               Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
                                     90
                                                          95
               Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
105
                   100
               Arg Arg Arg Ser Arg Asn Leu/Gly Lys Val Ile Asp Thr Leu
                       115
                                             120
               Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                            130
                                                 135
         20
               Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
                                145
                                                     150
               Val Arg Val Leu Glu Asp Glly Val Asn Tyr Ala Thr Gly Asn
                                    160
                                                         165
               Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
                                        175
                   170
               Ser Cys Leu Thr Ile Pro Ala Ser Ala
         25
                       185
                                             190
               (2)
                     INFORMATION FOR SEQ ID NO:
                       (i)
                                SEQUENCE CHARACTERISTICS:
```

(A)

(B)

(C)

(D)

(A)

(C)

LENGTH:

TOPOLOGY:

ORIGINAL SOURCE:

TYPE: amino acid

OR GANISM: homosapiens

INDIVIDUAL ISOLATE:

STRANDEDNESS:

191 amino acids

unknown

unknown

35

30

0

5

(vi)

```
0
                      SEQUENCE DESCRIPTION: SEQ ID NO:
             (xi)
     Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
                                            10
     Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
                           20
     Gln Ile Val Gly Gly Val Tykr Leu Leu Pro Arg Arg Gly Pro
 5
     Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
                                    50
     Gln Pro Arg Gly Arg Arg GAn Pro Ile Pro Lys Ala Arg Arg
                   60
                                        65
     Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
10
     Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
                           90
     Ser Pro Arg Gly Ser Arg/Pro Ser Trp Gly Pro Thr Asp Pro
                              105
     Arg Arg Arg Ser Arg Asn/Leu Gly Lys Val Ile Asp Thr Leu
              115
                                   120
                                                        125
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                                       135
                  130
15
     Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
                      145
                                           150
     Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
                          160
                                               165
     Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
     Ser Cys Leu Thr Ile Fro Ala Ser Ala
              185
20
      (2)
            INFORMATION FOR SEQ ID NO:
             (i)
                      SEQUENCE CHARACTERISTICS:
                           LENGTH:
                      (A)
                                    191 amino acids
                      (B)
                           TYPE:
                                   amino acid
25
                      (C)
                           STRANDEDNESS: unknown
                      (D)
                           TOPOLOGY:
                                      unknown
                      ORIGINAL SOURCE:
             (vi)
                      (A)
                           ORGANISM:
                                       homosapiens
                      (C)
                            INDIVIDUAL ISOLATE:
                                                 DK1
             (xi)
                      SEQUENCE DESCRIPTION:
                                              SEQ ID NO:
30
     Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
                                            10
     Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
                                                25
     Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
           30
                                35
35
     372577 1
```

```
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
                                   50
     Gln Pro Arg Gly Arg Arg Gln
                                  Pro Ile Pro Lys Ala Arg Arg
     Pro Glu Gly Arg Ala Trp Ala
                                  Gln Pro Gly Tyr Pro Trp Pro
                                            80
     Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
5
                           90
     Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
         100
                              105
                                                   110
     Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
             115
                                  120
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                  130
                                      135
     Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
10
                      145
                                           150
     Val Arg Val Leu Glu Asp Gly | Val Asn Tyr Ala Thr Gly Asn
                          160
                                               165
     Leu Pro Gly Cys Ser Phe Ser/Ile Phe Leu Leu Ala Leu Leu
                              175
                                                   180
     Ser Cys Leu Thr Ile Pro Ala Ser Ala
             185
                                  190
15
```

(2) INFORMATION FOR SEQ 1D NO: 167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu 85 90 0 95

35

20

25

```
0
      Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
          100
                               105
                                                    110
      Arg Arg Arg Ser Arg Asn Leu Gty Lys Val Ile Asp Thr Leu
                                   120
              115
      Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                                       135
      Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 5
                      145
                                           150
      Val Arg Val Leu Glu Asp Gly Yal Asn Tyr Ala Thr Gly Asn
                           160
      Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
                               175
                                                    180
      Ser Cys Leu Thr Ile Pro Ala/Ser Ala
              185
                                   190
10
      (2)
            INFORMATION FOR SEQ ID NO:
             (i)
                      SEQUENCE CHARACTERISTICS:
                            LENGTH: 191 amino acids
                       (A)
                       (B)
                            TYPE: amino acid
                       (C)
                            STRANDEDNESS:
                                           unknown
15
                       (D)
                            TOPOLOGY:
                                       unknown
             (vi)
                      ORIGINAL SOURCE:
                       (A)
                            ORGANISM:
                                       homosapiens
                            INDIVIDUAL ISOLATE:
                       (C)
                                                  SW2
             (xi)
                      SEQUENÇE DESCRIPTION:
                                              SEQ ID NO:
                                                           168:
20
     Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
      Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
                                                 25
      Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
      Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
25
               45
                                    50
      Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
                   60
                                        65
      Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
                        75
                                             80
     Leu Tyr Gly Asn Glu $\psi$ly Met Gly Trp Ala Gly Trp Leu Leu
      Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
30
          100
                               105
     Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
              115
                                   120
                                                        125
      Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                  130
                                       135
      Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
                       145
35
```

```
Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 155

Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 170

Ser Cys Leu Thr Ile Pro Ala Ser Ala 185
```

5

10

)

- (2) INFORMATION FOR SEQ ID NO: | 169:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: INDE
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:
- 15 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 5 10 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 45 50 20 Gln Pro Arg Gly Arg Arg Gln Pro|Ile Pro Lys Ala Arg Arg 60 65 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu 90 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro 25 105 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120 125 Thr Cys Gly Phe Ala Asp Leu Met | Gly Tyr Ile Pro Leu Val 130 135 Gly Ala Pro Leu Gly Gly Ala Ala/Arg Ala Leu Ala His Gly 145 150 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 30 160 165

Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu

190

Ala

175

Ser Cys Leu Thr Ile Pro Ala Ser

35

170

٥								130						
	(2)	INFORMATION FOR SEQ ID NO: 170:												
5			(i)		SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown									
		(vi)		ORI((A) (C)	OR	GANI		homo	homosapiens ISOLATE: IND8					
			(xi)		SEQ	SEQUENCE DESCRIPTION:						ID NO	O: :	170:
10	Met 1	Ser	Thr	Asn	Pro 5	Lys	Pro	Gln	Arg	Lys 10	Thr	Lys	Arg	Asn
	Thr 15	Asn	Arg	Arg	Pro	Gln 20	Asp	Val	Lys		Pro 25	Gly	Gly	Gly
	Gln	Ile 30	Val	Gly	Gly	Val	Tyr 35	Leu	Leu	Pro		Arg 40	Gly	Pro
1.0	Arg	Leu	Gly 45	Val	Arg	Ala	Thr	Arg 50	Lys	Thr	Ser	Glu	Arg 55	Ser
15	Gln	Pro	Arg	Gly 60	Arg	Arg	Gln	Pro	Ile 65	Pro	Lys	Ala	Arg	Arg 70
					75			Gln		80			_	
	85	1				90		Gly			95			
20		100					109					110	_	
			115					Gly 120				_	125	
				130				Met	135					140
					145			Ala		150				_
25	155					160		Val			165			
		170					175	Ile		Leu	Leu	Ala 180	Leu	Leu
	Ser	Cys	Leu 185	Thr	Val	Pro	Ala	Ser 190	Ala					
30	(2)		NFORN	MATI(SEQU (A) (B) (C)									
35			(vi)		ORIC	SINAI	J SOT	JRCE:						

372577 1

(A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: (xi) SEQUENCE DESCRIPTION: SEO ID NO: 171: Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 5 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 20 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 30 35 Arg Leu Gly Val Arg Ala Thr Arg|Lys Thr Ser Glu Arg Ser 45 50 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg His 10 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro 75 80 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu 90 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro 100 105 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 15 115 120 125 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 130 135 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly 145 150 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 155 160 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 20 175 Ser Cys Leu Thr Ile Pro Ala Ser Ala 185 19b INFORMATION FOR SEQ ID NO: (2) 25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1191 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY unknown (vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens 30 (C) INDIVIDUAL ISOLATE: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172: Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 35

1,98 -Thr Asn Arg Arg Pro Gln Asp Wal Lys Phe Pro Gly Gly Gly 20 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 Gln Pro Arg Gly Arg Arg Gln/Pro Ile Pro Lys Ala Arg Gln 65 5 Pro Glu Gly Arg Thr Trp Ala/Gln Pro Gly Tyr Pro Trp Pro 75 80 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu 90 95 Ser Pro Arg Gly Ser Arg Prb Asn Trp Gly Pro Thr Asp Pro 100 10/5 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 10 120 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 135 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150 Val Arg Val Leu Glu Asp Ely Val Asn Tyr Ala Thr Gly Asn 160 165 Leu Pro Gly Cys Ser Phe/Ser Ile Phe Leu Leu Ala Leu Leu 15 170 175 Ser Cys Leu Thr Thr Pro/ Ala Ser Ala 185 (2) INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: (i) 20 (A) LENGTH: 191 amino acids (B) TYPE: amino acid (C) \$TRANDEDNESS: unknown (D) TOPOLOGY: unknown (vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens 25 (C) INDIVIDUAL ISOLATE: HK5 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 173: Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 10 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 20 25 30 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 35 Arg Leu Gly Val Arg|Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg 65 35

```
Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
     Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
                           90
     Ser Pro His Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
                              105
     Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
                                  120
5
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                                      135
                 130
     Gly Ala Pro Leu Gly Gly Val Ala Atg Ala Leu Ala His Gly
     Val Arg Val Leu Glu Asp Gly Val A$n Tyr Ala Thr Gly Asn
     155
                          160
                                              165
     Ile Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
10
         170
                              175
     Ser Cys Leu Thr Thr Pro Val Ser Ala
             185
                                  190
```

INFORMATION FOR SEQ ID NO: (2) 174:

	(i)	SEQUENCE	CHAR	ACTE	RISTICS:	
15		(A) LENC	· urr	191	amino	20

- (A) LENGTH: 191 amino acids
- (B) TYPE: amin¢ acid
- (C) STRANDEDNESS: unknown
- TOPOLOGY: (D) unknown
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: HK4
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 10 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 25 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 30 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 Gln Pro Arg Gly Arg Arg Gln Pro | Ile Pro Lys Ala Arg Gln Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro 75 80 30 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro

105 Arg Arg Arg Ser Arg Asn Leu Gly tys Val Ile Asp Thr Leu 120

35

15

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Val Ala Atg Ala Leu Ala His Gly 145 150 Val Arg Val Val Glu Asp Gly Val A\$n Tyr Ala Thr Gly Asn 160 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 175 5 Ser Cys Leu Thr Ile Pro Ala Ser Ala 185 190

(2) INFORMATION FOR SEQ ID NO:

(i) SEQUENCE CHARACTERISTICS: 10

19‡ amino acids (A) LENGTH:

(B) TYPE: aminb acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

> ORGANISM: (A) homosapiens

> ISOLATE: (C) INDIVIDUAL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Met Ser Thr Thr Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Ser Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 20 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 20 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 Gln Pro Arg Gly Arg Arg Gln Pro | Ile Pro Lys Ala Arg Arg 65 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly His Pro Trp Pro 25 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu 90 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro 100 105 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120

125 Thr Cys Gly Phe Ala Asp Leu Met/Gly Tyr Ile Pro Leu Val 130 135

Gly Gly Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150

Val Arg Val Val Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 160 165 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu

170 175

35

```
201
      Ser Cys Leu Thr Ile Pro Ala Ser
              185
                                   190
      (2)
            INFORMATION FOR SEQ ID NO:
             (i)
                      SEQUENCE CHARACTERISTICS:
                            LENGTH: 191 amino acids
                       (A)
 5
                                   amino acid
                       (B)
                            TYPE:
                       (C)
                            STRANDEDNESS:
                                           unknown
                            TOPOLOGY: unknown
                       (D)
             (vi)
                      ORIGINAL SOURCE:
                       (A)
                            ORGANISM:
                                       homosapiens
                       (C)
                            INDIVIDUAL ISOLATE:
10
             (xi)
                      SEQUENCE DESCRIPTION:
                                              SEQ ID NO:
      Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
                                            10
      Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
                            20
      Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
15
                                35
      Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
                                    50
               45
      Gln Pro Arg Gly Arg Arg Gln Pro |Ile Pro Lys Ala Arg Arg
                   60
                                        65
      Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
                        75.
      Leu Tyr Gly Asp Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
20
                            90
      Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Thr Asp Pro
                               105
      Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
              115
                                   120
                                                        125
      Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                  130
                                       135
25
      Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
                      145
                                           150
      Val Arg Val Leu Glu Asp Gly Val
                                       Asn Tyr Ala Thr Gly Asn
                           160
                                                165
     Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
          170
                               175
      Ser Cys Leu Thr Ile Pro Ala Ser Ala
              185
                                   190
30
      (2)
            INFORMATION FOR SEQ ID NO:
             (i)
                      SEQUENCE CHARACTERISTICS:
                       (A)
                            LENGTH:
                                    191 amino acids
                       (B)
                            TYPE:
                                   amilno acid
35
```

```
0
                       (C)
                            STRANDEDNESS:
                                           unknown
                       (D)
                            TOPOLOGY:
                                      unknown
             (vi)
                      ORIGINAL SOURCE!
                       (A)
                            ORGANISM:
                                       homosapiens
                       (C)
                            INDIVIDUAL
                                       ISOLATE:
 5
             (xi)
                      SEQUENCE DESCRIPTION:
                                              SEO ID NO:
                                                           177:
     Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
                                            10
      Thr Asn Arg Arg Pro Gln Asp Val
                                       Lys Phe Pro Gly Gly Gly
                            20
      Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
                                35
10
                                                     40
      Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
               45
                                    50
      Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
                                        65
      Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
      Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
15
                            90
      Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
          100
                               105
      Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
              115
                                   120
                                                        125
      Thr Cys Ser Leu Ala Asp Leu Met Gly Tyr Val Pro Val Val
                  130
                                       135
      Gly Gly Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
20
                      145
                                           150
     Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
                           160
                                                165
      Leu Pro Gly Cys Ser Phe Ser Iİe Phe Leu Leu Ala Leu Leu
          170
                               175
      Ser Cys Ile Thr Ile Pro Val Ser Ala
              185
                                   190
25
      (2)
            INFORMATION FOR SEQ ID NO:
             (i)
                      SEQUENCE CHARACTERISTICS:
                            LENGTH: 191 amino acids
                       (A)
                       (B)
                            TYPE:
                                   amino acid
                       (C)
                            STRANDEDNESS:
                                           unknown
                            TOPOLOGY: unknown
                       (D)
30
             (vi)
                      ORIGINAL SOURCE:
                       (A)
                            ORGANISM: homosapiens
                            INDIVIDUAL ISOLATE:
                       (C)
                      SEQUENCE DESCRIPTION:
             (xi)
                                              SEQ ID NO:
                                                           178:
35
```

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
                                           10
     Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
     Gln Ile Val Gly Gly Val Tyr Ļeu Leu Pro Arg Arg Gly Pro
     Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
5
                                   50
     Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
                                       65
     Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
     Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
10
     Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
                              105
     Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
                                  120
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
                  130
                                      135
     Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
                      145
                                          150
15
     Val Arg Val Leu Glu Asp Gly Wal Asn Tyr Ala Thr Gly Asn
                          160
                                              165
     Leu Pro Gly Cys Ser Phe Ser/Ile Phe Leu Leu Ala Leu Leu
                              175
     Ser Cys Ile Thr Ile Pro Val Ser Ala
             185
                                  190
20
```

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: | amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: T9
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

35

```
Gln Pro Arg Gly Arg Arg Glr Pro Ile Pro Lys Asp Arg Arg
                                        65
      Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
      Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
      Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Ser Asp Pro
 5
                               105
          100
                                                    110
      Arg His Arg Ser Arg Asn Vall Gly Lys Val Ile Asp Thr Leu
              115
                                   120
      Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
                                       135
      Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
                       145
      Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
10
                           160
                                                165
      Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
          170
      Ser Cys Ile Thr Thr Pro Ala Ser Ala
              185
                                   190
15
            INFORMATION FOR SEQ ID NO:
      (2)
                                         180:
             (i)
                      SEQUENCE CHARACTERISTICS:
                       (A)
                            LENGTH:
                                     191 amino acids
                       (B)
                            TY₽E:
                                   amino acid
                            STRANDEDNESS:
                       (C)
                                           unknown
                       (D)
                            TOPOLOGY:
                                       unknown
20
                      ORIGINAL SOURCE:
             (vi)
                       (A)
                            ORGANISM:
                                       homosapiens
                       (C)
                            INDIVIDUAL ISOLATE:
             (xi)
                      SEQUENCE DESCRIPTION:
                                              SEQ ID NO:
                                                           180:
      Met Ser Thr Ile Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
25
                                            10
      Thr Asn Arg Arg Pro Gin Asp Val Lys Phe Pro Gly Gly Gly
                                                 25
      Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
           30
      Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
                                    50
      Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
30
      Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
                       75
                                            80
     Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
                           90
      Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
          100
                               105
35
```

Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu 115 120 125 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val 130 135 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 5 160 165 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 170 175 Ser Cys Ile Thr Ile Pro Val Ser Ala 185 INFORMATION FOR SEQ ID NO: 10 (2)

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1/91 amino acids

(B) TYPE: amilno acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

15 (vi) ORIGINAL SOURCE:

> (A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:

Met Ser Thr Asn Pro Lys Pro Gin Arg Lys Thr Lys Arg Asn 20 10 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 20 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 30 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 45 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg 25 65 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro 75 80 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu 90 Ser Pro Arg Gly Ser Arg Pro Thr Trp Gly Pro Thr Asp Pro 100 105 110 Arg His Arg Ser Arg Asn Leu Gly Arg Val Ile Asp Thr Ile 30 120 115 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val

130 135 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn

155

Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 170 175 Ser Cys Phe Thr Val Pro Val Ser Ala

- (2)INFORMATION FOR SEQ ID NO: 182: 5
 - SEQUENCE CHARACTERISTICS: (i)
 - 191 amino acids (A) LENGTH:
 - (B) TYPE: amino acid
 - STRANDEDNESS: (C) unknown
 - (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE: 10
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL İSOLATE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 15 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 15 20 25 Gln Ile Val Gly Gly Val Tyr Leu/Leu Pro Arg Arg Gly Pro 30 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 45 50 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg 65 20 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro 75 80 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu 90

Trp Gly Pro Thr Asp Pro 100 105 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Ile 115 120 125

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val 130 135

Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150

Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn 155 160

Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 30 170 175 180

Ser Cys Ala Thr Val Pro Val Ser Ala 185 19b

Ser Pro Arg Gly Ser Arg Pro Thr

(2) INFORMATION FOR SEQ ID NO: 183:

35

25

```
(i)
                      SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH:
                                     191 amino acids
                      (B)
                           TYPE:
                                   amino acid
                      (C)
                           STRANDEDNES$: unknown
                      (D)
                           TOPOLOGY:
                                       unknown
             (vi)
                      ORIGINAL SOURCE:
 5
                      (A)
                           ORGANISM: homosapiens
                      (C)
                           INDIVIDUAL İSOLATE:
             (xi)
                      SEQUENCE DESCRIPTION: SEQ ID NO:
                                                           183:
     Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
10
     Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
                           20
     Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
     Arg Leu Gly Val Arg Thr Thr Arg Lys Thr Ser Glu Arg Ser
                                    50
     Gln Pro Arg Gly Arg Arg Gln Pro/Ile Pro Lys Asp Arg Arg
                                        65
                   60
15
     Ser Thr Gly Lys Pro Trp Gly Lys Pro Gly Tyr Pro Trp Pro
                       75
                                            80
     Leu Tyr Gly Asn Glu Gly Cys Gly
                                       Trp Ala Gly Trp Leu Leu
                           90
     Ser Pro Arg Gly Ser His Pro Asn Trp Gly Pro Thr Asp Pro
          100
     Arg His Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Ile
              115
                                   120
20
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
                                       135
     Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
                      145
                                           150
     Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
                          160
                                               165
     Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
25
          170
                               175
     Ser Cys Cys Thr Val Pro Val Ser Ala
              185
                                   190
      (2)
            INFORMATION FOR SEQ ID NO:
             (i)
                      SEQUENCE CHARACTERISTICS:
30
                      (A)
                           LENGTH: | 191 amino acids
                      (B)
                           TYPE:
                                  amino acid
                      (C)
                           STRANDEDNESS: unknown
                           TOPOLOGY:
                      (D)
                                       unknown
             (vi)
                      ORIGINAL SOURCE:
                      (A)
                           ORGANISM: homosapiens
35
```

(C) INDIVIDUAL ISOLATE: SW3 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184: Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 10 Thr Asn Arg Arg Pro Gln Asp Val|Lys Phe Pro Gly Gly Gly 5 20 25 Gln Ile Val Gly Gly Val Tyr Leu|Leu Pro Arg Arg Gly Pro 30 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg 65 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro 10 75 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu 90 Ser Pro Arg Gly Ser His Pro Asn Trp Gly Pro Thr Asp Pro 105 110 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Ile 115 120 125 15 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val 135 130 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn 155 160 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 170 175 20 Ser Cys Phe Thr Val Pro Val Ser Ala 190 (2) INFORMATION FOR SEQ ID NO: 185: (i) SEQUENCE CHARACTERISTICS: (A) 191 amino acids LENGTH: 25 (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown (vi) ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 20 25

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									1					
٥	Gln	Ile 30	Val	Gly	Gly	Val	Tyr 35	Leu	Leu	Pro	Arg	Arg 40	Gly	Pro
	Arg	Leu	Gly 45	Val	Arg	Ala	Thr	Arg 50	Lys	Ser	Ser	Glu	Arg 55	Ser
	Gln	Pro	Arg	Gly 60	Arg	Arg	Gln	Pro	Ile 65	Pro	Lys	Asp	Arg	Arg 70
5	Ser	Thr	Gly	Lys	Ser 75	Trp	Gly	Lys	Pro	Gly 80	Tyr	Pro	Trp	Pro
3	Leu 85	Tyr	Gly	Asn	Glu	Gly 90	Cys	Gly	Trp	Ala	Gly 95	Trp	Leu	Leu
	Ser	Pro 100	Arg	Gly	Ser	Arg	Pro 105	Thr	Trp	Gly	Pro	Thr 110	Asp	Pro
	Arg	His	Arg 115	Ser	Arg	Asn	Leu	Gly 120	Lys	Val	Ile	Asp	Thr 125	Ile
10	Thr	Cys	Gly	Phe 130	Ala	Asp	Leu	Met	Gly 135	Tyr	Ile	Pro	Val	Val 140
	Gly	Ala	Pro	Val	Gly 145	Gly	Val	Ala	Arg	Ala 150	Leu	Ala	His	Gly
	Val 155	Arg	Val	Leu	Glu	Asp 160	Gly	Ile	Asn	Tyr	Ala 165	Thr	Gly	Asn
	Leu	Pro 170	Gly	Cys	Ser	Phe	Ser 175	Ile	Phe	Leu	Leu	Ala 180	Leu	Leu
15	Ser	Cys	Cys 185	Thr	Val	Pro	Val	Ser 190	Ala					

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: S83
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 20 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 30 30 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg 65 70 Thr Thr Gly Lys Ser Trp Gly Arg Pro Gly Tyr Pro Trp Pro 75 80

35

•														
	Leu 85	Tyr	Gly	Asn	Glu	Gly 90	Leu	Gly	Trp	Ala	Gly 95	Trp	Leu	Leu
	Ser	Pro 100	Arg	Gly	Ser	Arg	Pro 105	Ser	Trp	Gly	Pro	Thr 110	Asp	Pro
	Arg	His	Lys 115	Ser	Arg	Asn	Leu	Gly 120	Lys	Val	Ile	Asp	Thr 125	Leu
5	Thr	Cys	Gly	Phe 130	Ala	Asp	Leu	Met	Gly 135	Tyr	Ile	Pro	Val	Val 140
	Gly	Ala	Pro	Val	Gly 145	Gly	Val	Ala	Arg	Ala 150	Leu	Ala	His	Gly
	Val 155	Arg	Val	Leu	Glu	Asp 160	Gly	Ile	Asn	Tyr	Ala 165	Thr	Gly	Asn
	Leu	Pro 170	Gly	Cys	Ser	Phe	Ser 175	Ile	Phe	Leu	Leu	Ala 180	Leu	Leu
10	Ser	Cys	Ile 185	Ser	Val	Pro	Val	Ser 190	Ala					

(2) INFORMATION FOR SEQ ID NO: 187:

```
(i)
         SEQUENCE CHARACTERISTICS:
```

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

> (A) ORGANISM: homosapiens

INDIVIDUAL ISOLATE: (C) HK10

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Met Ser Thr Leu Pro Lys Pro/Gln Arg Lys Thr Lys Arg Asn Thr Ile Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 15 20 25 Gln Ile Val Gly Gly Val Tyr Val Leu Pro Arg Arg Gly Pro 25 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 Gln Pro Arg Gly Arg Arg Glm Pro Ile Pro Lys Ala Arg Arg 65 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro 75 80 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu 30 90 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro

105 100 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120 125 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val

130

35

Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 150

Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn 155

Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe 170

Ser Cys Leu Ile His Pro Ala Ala Ser 190

(2) INFORMATION FOR SEQ ID NO: 188:

```
(i) SEQUENCE CHARACTERISTICS:
```

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: S5:
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10

Thr Ile Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20

Gln Ile Val Gly Gly Val Tyr Val Leu Pro Arg Arg Gly Pro
30 35 40

Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser

Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg

Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
75 80

Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu 85 90 95

Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Lou Cly Lyg Yel Ile Agn The Lou

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120 125

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 130 135 140 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly

145
150
Val Arq Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn

Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn
155
160
165

Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
170
175
180

Ser Cys Leu Val His Pro Ala Ala Ser 185

35

25

30

5

```
(2)
            INFORMATION FOR SEQ ID NO:
                                         189:
             (i)
                      SEQUENCE CHARACTERISTICS:
                       (A)
                            LENGTH:
                                    191 amino acids
                       (B)
                            TYPE:
                                   amino acid
 5
                       (C)
                            STRANDEDNESS:
                                           unknown
                       (D)
                            TOPOLOGY: unknown
             (vi)
                      ORIGINAL SOURCE:
                       (A)
                            ORGANISM: homosapiens
                       (C)
                            INDIVIDUAL ISOLATE:
             (xi)
10
                      SEQUENCE DESCRIPTION:
                                              SEO ID NO:
     Met Ser Thr Leu Pro Lys Pro Gin Arg Lys Thr Lys Arg Asn
                                            10
     Thr Ile Arg Arg Pro Gln Asp Ile Lys Phe Pro Gly Gly Gly
                            20
                                                 25
     Gln Ile Val Gly Gly Val Tyr Val Leu Pro Arg Arg Gly Pro
           30
                                35
15
     Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
               45
     Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
                   60
                                                             70
     Ser Glu Gly Arg Ser Trp Ala Glh Pro Gly Tyr Pro Trp Pro
                       75
                                            80
     Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
20
     Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
          100
                               105
     Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
              115
                                   12b
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                                       135
                  130
     Gly Ala Pro Val Gly Gly Val Ala Arq Ala Leu Ala His Gly
25
                      145
                                           150
     Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn
     155
                           160
                                                165
     Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
                               175
                                                    180
     Ser Cys Leu Ile His Pro Ala Ala Ser
                                   190
              185
30
      (2)
            INFORMATION FOR SEQ ID NO:
                                         190:
             (i)
```

SEQUENCE CHARACTERISTICS:

STRANDEDNESS:

191 amino acids

unknown

amino acid

LENGTH:

TYPE:

(A)

(B)

(C)

372577_1

```
0
                       (D)
                            TOPOLOGY:
                                       unknown
             (vi)
                      ORIGINAL SOURCE
                       (A)
                            ORGANISM:
                                       homosapiens
                       (C)
                            INDIVIDUAL | ISOLATE:
             (xi)
                      SEQUENCE DESCRIPTION: SEQ ID NO:
                                                           190:
 5
     Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
      Thr Ile Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
      Gln Ile Val Gly Gly Val Tyr Val Leu Pro Arg Arg Gly Pro
                                35
     Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
10
                                    50
      Gln Pro Arg Gly Arg Arg Gln Pro |Ile Pro Lys Ala Arg Arg
                                        65
      Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
     Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
                            90
15
      Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
          100
                               105
     Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
              115
                                   120
                                                        125
      Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                  130
                                       135
     Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
                      145
                                           150
20
     Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn
                           160
     Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
          170
                               175
      Ser Cys Leu Ile His Pro Ala Ala
                                       Ser
25
      (2)
            INFORMATION FOR SEO ID NO:
             (i)
                      SEQUENCE CHARACTERISTICS:
                       (A)
                                     191 amino acids
                            LENGTH:
                       (B)
                            TYPE:
                                   amino acid
                       (C)
                            STRANDEDNESS:
                                           unknown
                       (D)
                            TOPOLOGY:
                                      unknown
30
             (vi)
                      ORIGINAL SOURCE:
                       (A)
                            ORGANISM: homosapiens
                            INDIVIDUAL ISOLATE:
                       (C)
             (xi)
                      SEQUENCE DESCRIPTION: SEQ ID NO:
                                                           191:
35
```

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 10 Thr Asn Arg Arg Pro Met Asp Vall Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Let Leu Pro Arg Arg Gly Pro 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 5 50 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln 65 Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro 75 80 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu 90 10 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro 105 100 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120 Thr Cys Gly Phe Ala Asp Leu Met! Gly Tyr Ile Pro Ile Val 135 130 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150 15 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn 160 165 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 170 175 Ser Cys Leu Thr Val Pro Ala Ser Ala 19b 185 (2) INFORMATION FOR SEQ ID NO: 20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown 25 (vi) ORIGINAL SOURCE: ORGANISM! homosapiens (A) (C) INDIVIDUAL ISOLATE: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192: Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 30 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly 20 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 35 40 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50

214

35

```
Gln Pro Arg Gly Arg Arg Gln Pro | Ile Pro Lys Ala Arg Arg
                                       65
     Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
     Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
                           90
     Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
                              105
5
     Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
             115
                                  120
                                                       125
     Thr Cys Gly Phe Ala Asp Leu Met Gḷy Tyr Ile Pro Leu Val
     Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
                     145
                                          150
     Val Arq Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
10
                          160
     Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
         170
                              175
     Ser Cys Leu Thr Val Pro Ala Ser Ala
```

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- 20 (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: Z1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10

Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
15 20 25

Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro

30 35 40
Arg Leu Gly Val Arg Ala Ala Arg Lys Thr Ser Glu Arg Ser

45 50 55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg

Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro

75
Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
85
90
95

Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro 100 105 110

35

216 -Arq Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 130 135 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn 160 165 5 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu 175 Ser Cys Leu Thr Thr Pro Ala Ser Ala 185 190 (2) INFORMATION FOR SEQ ID NO: 10 (i) SEQUENCE CHARACTERISTICS: LENGTH: 191 amino acids (A) (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown (vi) ORIGINAL SOURCE: 15 (A) ORGANISM: | homosapiens (C) INDIVIDUAL ISOLATE: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194: Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Met Asp Vall Lys Phe Pro Gly Gly Gly 20 20. Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 35 30 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Gln Ala Arg Arg 60 65 25 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro 75 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu 90 Ser Pro Arg Gly Ser Arg Pro S¢r Trp Gly Gln Asn Asp Pro 105 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 120 115 30 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 130 135 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150 Val Arg Ala Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn 155 160 165

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Leu Pro Gly Cys Ser Phe Ser | Ile Phe Leu Leu Ala Leu Phe
                               175
                                                    180
      Ser Cys Leu Thr Thr Pro Ala
                                   Ser Ala
              185
                                   190
      (2)
            INFORMATION FOR SEQ ID \ NO:
 5
             (i)
                      SEQUENCE CHARACTERISTICS:
                       (A)
                           LENGTH: | 191 amino acids
                       (B)
                                   amino acid
                            TYPE:
                       (C)
                            STRANDEDNESS:
                                           unknown
                            TOPOLOGY: unknown
                       (D)
             (vi)
                      ORIGINAL SOURCE:
10
                            ORGANISM: homosapiens
                       (A)
                            INDIVIDUAL ISOLATE:
                       (C)
             (xi)
                      SEQUENCE DESCRIPTION: SEQ ID NO:
     Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
                                            10
      Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
15
                            20
                                                 25
      Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
           30
                                35
      Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
      Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
                   60
                                        65
      Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
20
     Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
                            90
      Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
                               105
                                                    110
     Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
              115
                                   120
25
      Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                                       135
     Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
                      145
                                           150
     Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
     155
                           160
     Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
          170
                               175
30
      Ser Cys Leu Thr Val Pro Thr
                                   Ser Ala
                                   190
      (2)
            INFORMATION FOR SEQ ID NO:
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SEQUENCE CHARACTERISTICS:

372577_1

35

(i)

```
0
                       (A)
                           LENGTH:
                                    191 amino acids
                       (B)
                            TYPE:
                                   amino acid
                            STRANDEDNESS: unknown
                       (C)
                            TOPOLOGY:
                       (D)
                                       unknown
                      ORIGINAL SOURCE:
             (vi)
                            ORGANISM: homosapiens
 5
                       (C)
                            INDIVIDUAL ISOLATE:
             (xi)
                      SEQUENCE DESCRIPTION:
                                              SEQ ID NO:
                                                           196:
     Met Ser Thr Asn Pro Lys Pro $ln Arg Lys Thr Lys Arg Asn
                                            10
      Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
10
                            20
      Gln Ile Val Gly Gly Val Tyr ‡eu Leu Pro Arg Arg Gly Pro
           30
                                35
      Arg Leu Gly Val Arg Thr Thr Arg Lys Thr Ser Glu Arg Ser
                                    50
               45
      Gln Pro Arg Gly Arg Arg Gln Þro Ile Pro Lys Ala Arg Arg
                   60
                                        65
                                   Gln Pro Gly Tyr Pro Trp Pro
      Ser Glu Gly Arg Ser Trp Ala
15
                       75
                                            80
     Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
                            90
                                                 95
      Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
                               105
                                                    110
      Arg Arg Arg Ser Arg Asn Leu | Gly Lys Val Ile Asp Thr Leu
              115
                                   120
      Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
20
                  130
                                       135
      Gly Ala Pro Val Gly Gly Va∐ Ala Arg Ala Leu Ala His Gly
                      145
                                            150
     Val Arg Ala Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
                           160
                                               165
     Leu Pro Gly Cys Ser Phe Set Ile Phe Leu Leu Ala Leu Leu
          170
                               175
25
      Ser Cys Leu Thr Val Pro Ala Ser Ala
              185
                                   190
      (2)
            INFORMATION FOR SEQ ID NO:
             (i)
                      SEQUENCE CHARACTERISTICS:
                       (A)
                           LENGTH: 191 amino acids
30
                       (B)
                            TYPE: amino acid
                       (C)
                            STRANDEDNESS:
                                           unknown
                       (D)
                            TOPOLOGY: unknown
                      ORIGINAL SOURCE:
             (vi)
                           ORGANISM: homosapiens
                       (A)
                       (C)
                            INDIVIDUAL ISOLATE: DK13
35
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0 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197: Met Ser Thr Asn Pro Lys Pro Glin Arg Lys Thr Lys Arg Asn 10 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly 20 5 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arq Arq Gly Pro 30 35 Arg Leu Gly Val Arg Ala Thr A‡g Lys Thr Ser Glu Arg Ser 45 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln Leu Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro 10 75 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro 100 105 110 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val 15 130 135 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150 Val Arg Leu Leu Glu Asp Gly | Val Asn Tyr Ala Thr Gly Asn 155 160 165 Leu Pro Gly Cys Ser Phe Ser/Ile Phe Leu Leu Ala Leu Leu 175 Ser Cys Leu Thr Val Pro Ala Ser Ala 20 185 190 INFORMATION FOR SEQ ID NO: (2) (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 amino acids 25 (B) TYPE: amino acid (C) STRANDEDNESS: unknown TOPOLOGY: (D) unknown ORIGINAL SOURCE: (vi) (A) ORGANISM: homosapiens INDIVIDUAL ISOLATE: (C) 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198: Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 10 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly 20

219 -

35

- 220 Gln Ile Val Gly Gly Val Tyr Leu Pro Arg Arg Gly Pro 35 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln 60 65 Pro Thr Gly Arg Ser Trp Gly Glh Pro Gly Tyr Pro Trp Pro 75 5 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu 90 95 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro 105 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 10 130 135 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150 Val Arg Val Leu Glu Asp Gly Val| Asn Tyr Ala Thr Gly Asn 160 165 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu 170 175 Ser Cys Leu Thr Val Pro Ala Ser Ala 15 INFORMATION FOR SEQ ID NO: (2) (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 amino acids (B) TYPE: amino acid (C) STRANDEDNÉSS: unknown 20 (D) TOPOLOGY: unknown (vi) ORIGINAL SOURCE: ORGANISM: homosapiens (A) (C) INDIVIDUAL ISOLATE: SA5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25 Met Ser Thr Asn Pro Lys Pro Glin Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu Pro Arg Arg Gly Pro 30 35 Arg Leu Gly Val Arg Ala Thr A‡g Lys Thr Ser Glu Arg Ser 30 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln 65 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro 80 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu 85

372577_1

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- 221
 0
     Ser Pro Arg Gly Ser Arg Pro Ash Trp Gly Pro Asn Asp Pro
                               105
     Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
              115
                                   120
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                                       135
     Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 5
                      145
                                           150
     Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
     155
                          160
     Leu Pro Gly Cys Ser Phe Ser [le Phe Ile Leu Ala Leu Leu
                               175
     Ser Cys Leu Thr Val Pro Ala Ser Ala
                                   190
              185
10
      (2)
            INFORMATION FOR SEQ ID NO:
                                         200:
             (i)
                      SEQUENCE CHARACTERISTICS:
                                    191 amino acids
                       (A)
                           LENGTH:
                                  amino acid
                       (B)
                           TYPE:
                       (C)
                           STRANDEDNESS:
                                           unknown
15
                       (D)
                           TOPOLGGY:
                                       unknown
             (vi)
                      ORIGINAL SOURCE:
                           ORGANISM:
                       (A)
                                       homosapiens
                           INDIVIDUAL ISOLATE:
                                                 SA7
             (xi)
                      SEQUENCE DESCRIPTION:
                                              SEQ ID NO:
                                                           200:
20
     Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
                                            10
     Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
                           20
     Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
                                35
           30
     Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
25
               45
                                    50
     Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
                                        65
     Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
     Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
                           90
     Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
30
                               105
     Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
              115
                                   120
                                                        125
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                                       135
                  130
     Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
                      145
35
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Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 160 165 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu 170 175 Ser Cys Leu Thr Val Pro Ala Ser Ala 185

5

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- (2) INFORMATION FOR SEQ ID NO: 201:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:
- 15 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn 10 Thr Asn Leu Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro 35 40 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 20 Gln Pro Arg Gly Arg Arg Gln Pro | Ile Pro Lys Ala Arg Gln 60 65 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu 90 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro 25 105 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 130 135 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150

160 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu 170

185

175 Ser Cys Leu Ile Ile Pro Ala Ser Ala

Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn

19Ò

165

180

35

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INFORMATION FOR SEQ ID No:
      (2)
                                         202:
             (i)
                      SEQUENCE CHARACTERISTICS:
                                     191 amino acids
                       (A)
                           LENGTH:
                       (B)
                           TYPE:
                                   amino acid
                       (C)
                           STRANDEDNESS:
                                           unknown
                      (D)
                           TOPOLOGY:
                                       unknown
 5
             (vi)
                      ORIGINAL SOURCE
                      (A)
                           ORGANISM:
                                       homosapiens
                      (C)
                            INDIVIDUAL ISOLATE:
                                                 SA3
             (xi)
                      SEQUENCE DESCRIPTION: SEQ ID NO:
                                                           202:
     Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
10
     Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
                           20
     Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
                                35
     Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
               45
                                    50
                                                         55
15
     Gln Pro Arg Gly Arg Arg Gln Pro/Ile Pro Lys Ala Arg Gln
                   60
                                        65
                                                             70
     Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
                                            80
     Leu Tyr Ala Asn Glu Gly Leu Glu Trp Ala Gly Trp Leu Leu
     Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
          100
                               105
20
     Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
              115
                                   120
                                                        125
     Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
                  130
                                       135
     Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
                      145
                                           150
     Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
25
     155
                          160
     Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
                               175
                                                    180
     Ser Cys Leu Thr Val Pro Ala Ser Ala
                                   190
              185
     (2)
            INFORMATION FOR SEQ ID NO:
30
             (i)
                      SEQUENCE CHARACTERISTICS:
                           LENGTH:
                                    191 amino acids
                      (A)
                                   amino acid
                      (B)
                           TYPE:
                      (C)
                           STRANDEDNESS: unknown
                      (D)
                           TOPOLOGY: unknown
```

0		
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA13
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 203:
5	Met Ser Thr Asn	Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
	Thr Asn Arg Arg	Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
		Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
		Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
10	Gln Pro Arg Gly	Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln 65 70
		Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro 75 80
	85	Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu 90 95
16	100	Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
15	115	Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 120 125
	130	1
		Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150
20	155	Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 160 165
	170	Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu 175 180
	ser Cys Leu Thr 185	Val Pro Thr Ser Ala 190
	(2) INFORMATI	ON FOR SEQ ID NO: 204:
25	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown
30	(vi)	ORIGINAL SOURCE (A) ORGANISM: homosapiens (C) INDIVIDUAL ISOLATE: SA6
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 204:
35	Met Ser Thr Asn	Pro Lys Pro Gln Arg Lys Thr Gln Arg Asn 5
	372577 1	

Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Led Leu Pro Arg Arg Gly Pro 35 Arg Met Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser 50 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln 5 65 Ser Ala Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro 100 105 10 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu 115 120 125 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val 130 135 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 145 150 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn 155 160 165 15 Leu Pro Gly Cys Ser Phe Ser Ile Phe Val Leu Ala Leu Leu 175 Ser Cys Leu Thr Val Pro Ala Ser Ala 185 190

(2) INFORMATION FOR SEQ ID NO: 205:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: | homosapiens
 - (C) INDIVIDUAL ISOLATE: SA11
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

35

							-	226	-					
0														
	Pro	Thr	Gly	Arg	Ser 75	Trp	Gly	Gln	Pro	Gly 80	Tyr	Pro	Trp	Pro
	Phe 85	Tyr	Ala	Asn	-	Gly 90	Leu	Gly	Trp		Gly 95	Trp	Leu	Leu
		Pro 100	Arg	Gly	Ser	Arg	Pro 105	Asn	Trp	Gly	Pro	Asn 110	Asp	Pro
5	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly 120	Lys	Val	Ile	Asp	Thr 125	Leu
	Thr	Cys		Phe 130	Ala	Asp	Leu		Gly 135	Tyr	Ile	Pro	Leu	Val 140
	Gly	Gly	Pro	Val	Gly 145	Gly	Val	Ala	Arg	Ala 150	Leu	Ala	His	Gly
	Val 155	Arg	Ala	Leu	Glu	Asp 160	Gly	Vail	Asn	Tyr	Ala 165	Thr	Gly	Asn
10		Pro 170	Gly	Cys	Ser		Ser 175	Ile	Phe	Ile		Ala 180	Leu	Leu
	Ser	Cys	Leu 185	Thr	Val	Pro	Ala	Thr 190	Ala					
	(2)	II	NFORI	ITAN	ON FO	OR SI	EQ II	ON CO	: 20	06:				
15			(i)		SEQU (A) (B) (C) (D)	LEI TYI STI	E CHANGTH PE: RANDI	: 19 amir EDNES	91 ar	nino cid unkı	acio	ds		
20			(vi)		ORIO (A) (C)	ORG	SOUS SANIS	БМ:	homo	osap: LATE		K2		
			(xi)		SEQU	JENCI	E DES	SCRII	RIPTION: SEQ ID NO:				0: 2	206:
	Met 1	Ser	Thr	Leu	Pro 5	Lys	Prø	Gln	Arg	Lys 10	Thr	Lys	Arg	Asn
	Thr 15	Asn	Arg	Arg	Pro	Thr 20	Asp.	Val	Lys	Phe	Pro 25	Gly	Gly	Gly
25	Gln	Tle 30	Val	Gly	Gly	Val	Tyr 35	Leu	Leu	Pro	Arg	Arg 40	Gly	Pro
	Arg		Gly 45	Val	Arg	Ala	Thr	Arg 50	Lys	Thr	Ser		Arg 55	Ser
	Gln	Pro	Arg	Gly 60	Arg	Arg	Gln	Pro	Ile 65	Pro	Lys	Ala	Arg	Gln 70
20	Pro	Gln	Gly	Arg	His 75	Trp	Ala	Gln	Pro	Gly 80	Tyr	Pro	Trp	Pro
30	Leu 85	Tyr	Gly	Asn		Gly 90	¢уѕ	Gly	Trp		Gly 95	Trp	Leu	Leu
		Pro 100	Arg	Gly	Ser		Pro 105	His	Trp	Gly		Asn 110	Asp	Pro
					_	3	4	~7	T	TT - 7			_	
	Arg	Arg	Arg 115	Ser	Arg	Asn	Leu	120	туѕ	vaı	ile	Asp	Thr 125	Leu

							1							
0	Thr	Cys Gly	/ Phe 130		Asp	Leu	Met	Gly 135	Tyr	Ile	Pro	Val		
	Gly	Ala Pro		Gly	Gly	Val	Ala			Leu	Ala	His	140 Gly	
		Arg Ala	a Ile	145 Glu		Gly	Ile	Asn	150 Tyr		Thr	Gly	Asn	
		Pro Gly	y Cys	Ser	160 Phe		Ile	Phe	Leu	165 Leu		Leu	Leu	
5		170 Cys Le: 189		Thr	Pro	175 Ala	Ser 190	Ala			180			
	(2)	INFOR	OITAN	N FO	R SE	Q ID	NO:	207:						
10		(i)			LENO TYP: STR	GTH: E: 1	40 nuçl DNES	base eic a	pai: acid sing:	rs				
		(xi)		SEQU!	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	207:		
15	GCGT	CCGGGT	TCTG	GAAG	AC G	GCGT	GAAC	T AT	GCAA(CAGG				40
	(2)	INFOR	OITAN	N FO	R SE	Q ID	NO:	208:						
20		(i)		SEQU (A) (B) (C) (D)	LENO TYP:	GTH: E: : ANDE	40 nucl DNES	base eic a S:	pai: acid sing:	rs				
		(xi)	•	SEQU!	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	208:		
	AGGC	TTTCAT	TGCA	GTTC	AA G	GCCG'	TGCT.	A·TT(GATG'	TGCC				40
25	(2)	INFOR	OITAN	N FO	R SE	Q ID	NO:	209:						
		(i)		SEQU: (A) (B) (C) (D)	LENO TYP: STR.	GTH:	40 nucl DNES	base eic a	pai: acid sing:	rs				
30		(xi)		SEQU!	ENCE	DES	 CRIP	TION	: SE	Q ID	NO:	209:		
	AAGA	CGGCGT	GAAC	TATG	CA A	CAGG	GAAC	C TT	CCTG	GTTG				40
35	(2)	INFORM	OITAN	N FO	R SE	Q ID	NO:	210:						
							1							

0				
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:210:	
	AGTTO	CAAGGC CGT	GCTATTG ATGTGCCAAC TGCCGTTGGT	40
	(2)	INFORMATIO	ON FOR SEQ ID NO 211:	
10		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:211:	
15	AAGAC	CGGCGT GAA	TTCTGCA ACAGGGAACC TTCCTGGTTG	40
	(2)	INFORMATIO	ON FOR SEQ ID NO:212:	
20		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:212:	·
	AGTTO	CAAGGC CGTO	GGAATTC ATGTGCCAAC TGCCGTTGGT	40
25	(2)	INFORMATIO	ON FOR SEQ ID NO:213:	
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:213:	
	ARCTY	CGACG TYA	CATCGAY CTGCTYGTYG GRAGYGCCAC CC	42
	(2)	INFORMATIO	ON FOR SEQ ID NO:214:	
35				
	372577 1		1	

			- 229 -	
0				
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:214:	
	RCAR	GCCRTC TTG	GAYATGA TCGCTGGWGC Y	.31
	(2)	INFORMATIO	ON FOR SEQ ID NO:215:	
10		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:215:	
15	CRATA	ACGACR YCA	YGTCGAY TTGCTCGTTG GGGCGGCTRY YT	42
	(2)	INFORMATIO	ON FOR SEQ ID NO: 216:	
20		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:216:	
	RCAA	GCTRTC RTG	GAYRTGG TRRCRGGRGC C	31
25	(2)	INFORMATIO	ON FOR SEQ ID NO:217:	
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:217:	
-	TTGC	GGACKC ACA	TYGACAT GGTYGTGATG TCCGCCACGC	40
35	(2)	INFORMATIO	ON FOR SEQ ID NO:218:	
	372577 1			

0				
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:218:	
	GATGO		GAGGTCA TCWTAGACAT CRTYRGCGGR GCD	43
	(2)	INFORMATIO	ON FOR SEQ ID NO:219:	
10		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:219:	
15	AATGO ACAC	GCACCY TGC	RCTGCTG GATACAAGTR ACACCTAATG TGGCTGTGAA	50 54
	(2)	INFORMATIO	ON FOR SEQ ID NO:220:	
20		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:220:	
	TGAR	CTAGYC CTYS	SARGTYG TCTTCGGYGG Y	31
25	(2)	INFORMATIO	ON FOR SEQ ID NO:221:	
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
30		(!)	(D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:221:	
	GCCAA TCAA	ACGTCT CTC	GATGTTG GGTGCCGGTT GCCCCCAATC TCGCCATAAG	50 54
35			·	
	372577_1			

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Ü	(2)	INFORMATIO	ON FOR SEQ ID NO:222:	
5		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:222:	
	AAGG	GCCTGC GAG	CACACAT CGATATCATC GTGATGTCTG CTACGG	46
10	(2)	INFORMATIO	ON FOR SEQ ID NO: 223:	
10		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
15		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:223:	
	TTGG:	IGCGCA TCC	CGGAAGT CATCTTGGAT ATTGTTACAG GAGGT	45
	(2)	INFORMATIO	ON FOR SEQ ID NO:224:	
20		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: \(\) 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:224:	
25	AGTC	AGGTAY GTC	GGAGCAA CCACCGCYTC GATACGCAGT	40
	(2)	INFORMATIO	ON FOR SEQ ID NO:225:	
30		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:225:	
	AGCC'	TTCACG TTC	AGACCKC GTCGCCATCA AACRGTCCAG ACCTGT	46
35				
	372577_1			

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	(2)	INFORMATI	ON FOR SEQ ID NO: 226:	
5		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:226:	
			GTATGGT GGTRGCGCAC RTYCTGCGDY TGCCCCAGAC MTRGCYG GGGCC	50 75
10	(2)	INFORMATI	ON FOR SEQ ID NO 227:	
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
15		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:227:	
	ACGC	CGGTGA CGC	CCTACAGT GGCTGTCGCA CACCCGGGC	39
	(2)	INFORMATI	ON FOR SEQ ID NO:228:	
20		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:228:	
25 .	ATGA	GGGTCC CCA	CAGCCTT TCTCGACATG GTTGCCGGAG GC	42
	(2)	INFORMATI	ON FOR SEQ ID NO:229:	
30		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:229:	
	CGCG	CCCTAT CCC	CAACGCAC CGTTAGAGTC CATGCGCAGG	40
35				

0			- 233 -	
	(2)	INFORMAT	ION FOR SEQ ID NO:230:	
5		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 49 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:230:	
	TCAG	ATCTTA CGO	GATCCCCT CTATCCTAGG TGACTTGCTC ACCGGGGGT	49
10	(2)	INFORMAT	ION FOR SEQ ID NO:231:	
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
15		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:231:	
	CAGT CGGT		rgggtggc ccttactccc accgtggcgg ygycttatat	50 54
20	(2)	INFORMAT	ION FOR SEQ ID No:232:	
20		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:232:	•
23	TAGC.	ACTCTG GT	RGAYCTAC TCRCTGGAGG G	31
	(2)	INFORMAT	ION FOR SEQ ID NO:233:	
30		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:233:	
35	AAGT	CTACAT GC	GGGTGTC TCTCACCCCC ACCGTGGCTG CGCAACATCT	50
	272577 1			

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			234	
_			- 234 -	
0	GAAT			54
	(2)	INFORMATIO	ON FOR SEQ ID NO:234:	
5		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:234:	
10	AGGC	GCCATG GTC	GACCTGC TTGCAGGCGG C	31
10	(2)	INFORMATIO	ON FOR SEQ ID NO:235:	
15		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
15		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:235:	
	TCAGO	CCCCGA VYY	TCGGAGC GGTCACGGCT CCTCTTCGGA GGG	43
	(2)	INFORMATIO	ON FOR SEQ ID NO 236:	
20		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:236:	
23	TGYT	ACGGAT YCC	CCARGTG GTCATHGACA TCATWGCCGG GGSC	44
	(2)	INFORMATIO	ON FOR SEQ ID NO:237:	
30		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:237:	
35	CATAC	CCAAAT GCT	TCCACGC CCGCAACGGG ATTCCGCAGG	40
	372577_1			

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	(2)	INFORMAT	ION FOR	SEQ ID	ио: 238:					
5		(i)	(A) (B) (C)	NCE CHAR LENGTH: IYPE: n STRANDED IOPOLOGY	37 base ucleic a NESS: s	pairs cid single				·
		(xi)	SEQUE	NCE DESC	RIPTION:	SEQ ID	NO:2	38:		
	TCT	CTTGCG GG	CGCCGCA	G TGGTTT	GCTC ATC	CCTG				37
10	(2)	INFORMAT	ION FOR	SEQ ID	NO:239:					
		(i)	(A) 1 (B) 5 (C) 5	NCE CHAR LENGTH: TYPE: n STRANDED TOPOLOGY	52 base ucleic a NESS: s	pairs cid single				
15		(xi)	SEQUE	NCE DESC	RIPTION:	SEQ ID	NO:2	39:		
	ATC: GC	TAGCATC TTO				CGAGTGTG	ATAT	TTGO	GTG	50 52
20		(i)	SEQUEI (A) I (B) I	NCE CHAR LENGTH: IYPE: a STRANDED	ACTERIST 33 amino mino aci NESS: u	acids .d .nknown				
25		(xi)	SEQUE	NCE DESC	RIPTION:	SEQ ID	NO:2	240:		
	Trp	Ile Gln V	al Thr	Pro Asn	Val Ala	Val Lys	His	Arg	Gly	Ala 15
	Leu	Thr His A	-	Arg Xaa	His Xaa		Ile	Val	Met	
	Ala	Thr Val								30
30	(2)	INFORMAT	ION FOR	SEQ ID	NO:241:					
35		(i)	SEQUEI (A) I (B) I	NCE CHAR LENGTH:	ACTERIST 33 amino mino aci NESS: u	acids .d nknown				

SEQUENCE DESCRIPTION: SEQ ID NO:241: (xi) Trp Val Pro Val Ala Pro Asn Leu Ala Ile Ser Gln Pro Gly Ala 10 Leu Thr Lys Gly Leu Arg Ala His Ile Asp Ile Ile Val Met Ser 5 Ala Thr Val (2) INFORMATION FOR SEQ ID NO: 242: (i) SEQUENCE CHARACTERISTICS: LENGTH: 33 amino acids 10 (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242: Trp Ile Pro Val Xaa Pro Asn Val! Ala Val Xaa Xaa Pro Gly Ala 10 15 Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val Met Ser Ala Thr Leu (2) INFORMATION FOR SEQ ID NO: 243: (i) SEQUENCE CHARACTERISTICS: 20 (A) LENGTH: 33 amino acids (B) TYPE: amino acid (.C.) STRANDEDNESS: unknown TOPOLOGY: (D) unknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243: 25 Trp Thr Xaa Val Thr Pro Thr Val Ala Val Arg Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly Ala Ala Thr Xaa (2) INFORMATION FOR SEQ ID NO:244: 30 (i) SEQUENCE CHARACTERISTICS: LENGTH: 33 amino acids (A)

35

(B)

(C)

(D)

TYPE:

TOPOLOGY:

amino acid

unknown

STRANDEDNESS: unknown

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(xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:244:
      Trp Val Ala Leu Xaa Pro Thr Leu Ala Ala Arg Asn Xaa Xaa
                                             10
      Xaa Thr Xaa Xaa Ile Arg Xaa His Val Asp Leu Leu Val Gly Ala
                        20
      Ala Xaa Phe
 5
           INFORMATION FOR SEQ ID NO:245:
      (2)
                     SEQUENCE CHARACTERISTICS:
           (i)
                      (A)
                           LENGTH: 33 amino acids
                      (B)
                           TYPE:
                                 amino acid
10
                      (C)
                           STRANDEDNESS:
                                          unknown
                           TOPOLOGY:
                      (D)
                                      unknown
                     SEQUENCE DESCRIPTION: SEQ ID NO:245:
           (xi)
      Trp Val Xaa Xaa Xaa Pro Thr Val Ala Thr Arg Asp Gly Lys Leu
      Pro Xaa Xaa Gln Leu Arg Arg Xaa Ile Asp Leu Leu Val Gly Ser
15
                        20
      Ala Thr Leu
      (2)
           INFORMATION FOR SEQ ID NO:246:
           (i)
                     SEQUENCE CHARACTERISTICS:
                      (A)
                           LENGTH: 33 amino acids
                      (B)
                           TYPE: amino acid
20
                      (C)
                           STRANDEDNESS:
                                          unknown
                      (D)
                           TOPOLOGY:
                                      unknown
           (xi)
                     SEQUENCE DESCRIPTION: SEQ ID NO:246:
      Trp Thr Pro Val Thr Pro Thr Val Ala Val Ala His Pro Gly Ala
                                             10
25
      Pro Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala
     Ala Thr Leu
      (2)
           INFORMATION FOR SEQ ID NO:247:
           (i)
                     SEQUENCE CHARACTERISTICS:
30
                           LENGTH: 33 amino acids
                      (A)
                      (B)
                           TŸPE:
                                  amino acid
                           STRANDEDNESS: unknown
                      (C)
                      (D)
                           TOPOLOGY:
                                      unknown
                     SEQUENCE DESCRIPTION: SEQ ID NO:247:
           (xi)
35
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Trp Val Ala Leu Thr Pro Thr Val Ala Xaa Xaa Tyr Ile Gly Ala Pro Leu Xaa Ser Xaa Arg Arg His Val Asp Leu Met Val Gly Ala 20 Ala Thr Val 5 (2) INFORMATION FOR SEQ ID NO:248: SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 33 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:248: Trp Val Ser Leu Thr Pro Thr Val Ala Ala Gln His Leu Asn Ala 10 Pro Leu Glu Ser Leu Arg Arg His Val Asp Leu Met Val Gly Gly 20 Ala Thr Leu 15 (2) INFORMATION FOR SEQ ID NO:249: (i) SEQUENCE CHARACTERISTICS: LENGTH: 33 amino acids (A) TYPE ! (B) amino acid (C) STRANDEDNESS: unknown 20 (D) TOPOLOGY: unknown SEQUENCE DESCRIPTION: SEQ ID NO:249: (xi) Trp Val Pro Leu Thr Pro/Thr Val Ala Ala Pro Tyr Pro Asn Ala 10 Pro Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala 25 20 Ala Thr Met (2) INFORMATION FOR SEQ ID NO:250: SEQUENÇE CHARACTERISTICS: (i) (A) LENGTH: 33 amino acids 30 TYPE: amino acid (B) (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

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							_	239	_						
0	Trp	Val	Xaa	Ile	_	Pro	Thr	Leu	Ser		Pro	Xaa	Xaa	Gly	
	Val	Thr	Ala	Pro		Arg	Arg	Xaa	Val		Tyr	Leu	Ala	Gly	
	Ala	Ala	Leu		20					25					30
	(2)	IN	FORM	ATIO	N FOI	R SE	Q ID	NO:	251:						
5		(i)		SEQUI (A) (B) (C) (D)	LENG TYPI STRA	GTH:	33 a amino ONES	amino	o ac: id unkno	ids				
10		(x	i)	:	SEQUI	ENCE	DESC	CRIP	rion	: SEQ	Q ID	NO:2	251:		
10	Trp	His	Ala	Val	Thr 5	Pro	Thr	Leu	Ala	Ile 10	Pro	Asn	Ala	Ser	Thr
	Pro	Ala	Thr	Gly	_	Arg	Arg	His	Val		Leu	Leu	Ala	Gly	
	Ala	Val	Val		20					23					30
15	(2)	IN	FORM?	OITA	N FOI	R SEÇ	Q ID	NO : 2	252:						
20		(i))		SEQUI (A) (B) (C) (D)	LENC TYPI STRA	GTH	23 a amino ONES	amino	o ac: id unkno	ids				·
20		(x:	i)	:	SEQUI	ENCE	DESC	CRIP	CION	: SE(Q ID	NO:2	252:		
	Thr	Leu	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Ala	Arg	Val	Pro	Glu	Leu
25	Xaa	Leu	Xaa	Val	5 Val 20	Phe	Gly	Gly		10					. 15
25	(2)	IN	FORM	ATIO	N FOI	R SEÇ	ID	NO:2	253:						
30		(i))		SEQUI (A) (B) (C) (D)	LENC TYPE STR	GTH:	23 a amino ONESS	amino	o aci id unkno	ids				
		(x:	i)	Š	SEQUE	ENCE	DESC	CRIPT	CION	: SEÇ	Q ID	NO:2	253:		
	Thr	Thr	Thr	Met	Leu	Leu	Ala	Tyr	Leu		Arg	Ile	Pro	Glu	
35	Ile	Leu	Asp	Ile	Val 20	Thr	Gly	Gly		10					15
	372577_	.1										`			

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	(2) INFORMATION FOR SEQ ID NO:254:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 23 amino acids
5	(B) TYPE: amino acid (C) STRANDEDNESS: unknown
3	(D) TOPOLOGY: unknown
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:
	Thr Xaa Thr Xaa Ile Leu Ala Tyr Xaa Met Arg Val Pro Glu Val
10	Ile Xaa Asp Ile Xaa Xaa Gly Ala
	(2) INFORMATION FOR SEQ ID NO:255:
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 amino acids
	(B) TYPE: amind acid (C) STRANDEDNES\$: unknown
15	(D) TOPOLOGY: unknown
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:
	Ala Val Gly Met Val Val Ala His Xaa Leu Arg Leu Pro Gln Thr
20	Xaa Phe Asp Ile Xaa Ala Gly Ala
	(2) INFORMATION FOR SEQ ID NO:256:
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 amino acids
25	(B) TYPE: amino acid
23	(C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:
	Thr Xaa Ala Leu Val Xaa Ser Gln Leu Leu Arg Xaa Pro Gln Ala 5 10 15
30	Xaa Xaa Asp Xaa Val Xaa Gly Ala
	20
	(2) INFORMATION FOR SEQ ID NO:257:
	(i) SEQUENCE CHARACTERISTICS:
35	(A) LENGTH: 23 amino acids
	372577_1

٥ (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: uhknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257: Thr Xaa Ala Leu Val Xaa Ala Gln Leu Leu Arg Xaa Pro Gln Ala 5 Xaa Leu Asp Met Ile Ala Gly Ala (2) INFORMATION FOR SEQ ID NO: 258: (i) SEQUENCE CHARACTERISTICS: 10 LENGTH: 23 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258: Thr Thr Thr Leu Leu Leu Ala Gli Ile Met Arg Val Pro Thr Ala 15 10 Phe Leu Asp Met Val Ala Gly Glý 20 (2) INFORMATION FOR SEQ ID No:259: SEQUENCE CHARACTERISTICS: (i) 20 (A) LENGTH: 23 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown TOPOLOGY: (D) unknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259: 25 Thr Thr Thr Leu Xaa Leu Ala Gln Val Met Arg Ile Pro Ser Thr 15 Leu Val Asp Leu Leu Xaa Gly Gly 20 (2) INFORMATION FOR SEQ ID NO:260: (i) SEQUENCE CHARACTERISTICS: 30 (A) LENGTH: 23 amino acids (B) TYPE: | amino acid (C) STRANDEDNESS: unknown TOPOLOGY: (D) unknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260: 35 372577_1

0 Thr Ala Thr Leu Val Leu Ala \$\frac{1}{2}\text{In Leu Met Arg Ile Pro Gly Ala Met Val Asp Leu Leu Ala Gly \$ly 20 INFORMATION FOR SEQ ID NO:261: 5 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 amino acids (B) amilno acid TYPE: (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261: Thr Ser Ala Leu Ile Met Ala Glm Ile Leu Arg Ile Pro Ser Ile Leu Gly Asp Leu Leu Thr Gly Gly 20 15 (2) INFORMATION FOR SEQ ID NO 262: (i) SEQUENCE CHARACTERISTICS: LENGTH: 23 amino acids (A) (B) TYPE: amiho acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262: Xaa Thr Ala Leu Xaa Met Ala Gln Xaa Leu Arg Ile Pro Gln Val Val Ile Asp Ile Ile Ala Gly Xaa 20 25 (2) INFORMATION FOR SEQ ID ND:263: (i) SEQUENCE CHARACTERISTICS: LENGTH: 23 amino acids (A) amino acid (B) TYPE: (C) STRANDEDNESS: unknown (D) TOPOLOGY unknown 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Thr Thr Thr Leu Val Leu Ser Ser Ile Leu Arg Val Pro Glu Ile

Cys Ala Ser Val Ile Phe Gly Gly

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